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1.	Your reference	P011367GB CTH
2.	Patent application number *(The Patent Office will fill in this part)*	**0109781.5** 20 APR 2001
3.	Full name, address and postcode of the or of each applicant *(underline all surnames)*	Oxford BioMedica (UK) Limited Medawar Centre Robert Robinson Avenue The Oxford Science Park Oxford OX4 4GA United Kingdom
	Patents ADP number *(if you know it)*	7223522001
	If the applicant is a corporate body, give the country/state of its incorporation	United Kingdom
4.	Title of the invention	VECTOR SYSTEM
5.	Name of your agent *(if you have one)*	**D YOUNG & CO**
	"Address for service" in the United Kingdom to which all correspondence should be sent (including the postcode)	**21 NEW FETTER LANE LONDON EC4A 1DA**
	Patents ADP number *(if you know it)*	**59006**

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11. I/We request the grant of a Patent on the basis of this application.

Signature

D YOUNG & CO
Agents for the Applicants

Date

20 Apr 2001

12. Name and daytime telephone number of person to contact in the United Kingdom — Charles Harding — 023 80719500

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VECTOR SYSTEM

FIELD OF THE INVENTION

The present invention relates to a vector system. In particular, the present invention relates to viral vector system capable of delivering a nucleotide sequence of interest ("NOI") to a target adipose tissue site.

BACKGROUND TO THE INVENTION

Adipose tissue has a major endocrine role in addition to its triglyceride storage role.

The most important endocrine role of adipose tissue is probably the secretion of leptin, however other factors such as sex steroids and glucocorticoids, peptide hormone precursors (eg angiotensinogen), complement factors, pro-inflammatory cytokines, interleukin 6, transforming growth factor-beta, tissue factor, plasminogen activator inhibitor-1 Aipo Q and adiponectin are also secreted. Aberrant function of this tissue is associated with diseases such as diabetes (related to low levels of leptin secretion).

The regulation or alteration of these secretory functions by gene delivery could be use to treat a varied range of diseases.

One problem with gene therapy approaches in the treatment of diseases associated with adipose tissue, is that differentiated cells, such as adipose tissue cells, are difficult to transfect and/or transduce.

Hence, it is desirable to find a mechanism for transient or stable transfer of regulated genes into adipose tissue cells.

Finally, it is desirable to provide a better therapeutic approach for the treatment and/or prevention of diseases associated with adipose tissue.

SUMMARY OF ASPECTS OF THE PRESENT INVENTION

The first aspect of the present invention relates to a novel use of a viral vector system for transducing a target adipose tissue site.

In this respect, it has been found that a particular type of viral vector system is capable of effectively transducing a target adipose tissue site.

Other aspects of the present invention are presented in the accompanying claims and in the following description and drawings. These aspects are presented under separate section headings. However, it is to be understood that the teachings under each section are not necessarily limited to that particular section heading.

ADVANTAGES

The use of a viral vector system to transduce an adipose tissue site is advantageous because:

(i) the adipose cells are long lived so that treatments may only be required infrequently;

(ii) adipose tissue cells have a good connection to the circulatory system, so products could be quickly and efficiently supplied to the target organs;

(iii) native adipose tissue cells can express the correct transport and processing functions so that it is more likely that functional proteins will be produced;

(iv) if a gene mutation is involved in the disease phenotype, then expression in the native tissue site may allow product regulation by native systems; and

(v) gross regulation of product production may to some extent be determined by the numbers of cells treated.

Other advantages are discussed and are made apparent in the following commentary.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to a new use of a viral vector system for transducing a target adipose tissue site.

Preferably the viral vectors of the present invention are recombinant viral vectors. Suitable recombinant viral vectors include but are not limited to adenovirus vectors, adeno-associated viral (AAV) vectors, herpes-virus vectors, lentiviral vectors, baculoviral vectors, pox viral vectors or parvovirus vectors (see Kestler *et al* 1999 Human Gene Ther 10(10):1619-32).

In one embodiment of the present invention, a lentiviral vector is used to transduce a target adipose tissue site. A lentiviral vector belongs to the family of viral vectors known as retroviruses.

RETROVIRUSES

The concept of using retroviral vectors for gene therapy and gene delivery is well known (Verma and Somia (1997) Nature 389:239-242).

There are many retroviruses. For the present application, the term "retrovirus" includes: murine leukemia virus (MLV), human immunodeficiency virus (HIV), equine infectious anaemia virus (EIAV), mouse mammary tumour virus (MMTV), Rous sarcoma virus (RSV), Fujinami sarcoma virus (FuSV), Moloney murine leukemia virus (Mo-MLV), FBR murine osteosarcoma virus (FBR MSV), Moloney murine sarcoma virus (Mo-MSV), Abelson murine leukemia virus (A-MLV), Avian myelocytomatosis virus-29 (MC29), and Avian erythroblastosis virus (AEV) and all other retroviridiae including lentiviruses.

A detailed list of retroviruses may be found in Coffin *et al* ("Retroviruses" 1997 Cold Spring Harbour Laboratory Press Eds: JM Coffin, SM Hughes, HE Varmus pp 758-763).

In a preferred embodiment, the retroviral vector system is derivable from a lentivirus. Lentiviruses also belong to the retrovirus family, but they can infect both dividing and non-dividing cells (Lewis et al (1992) EMBO J. 3053-3058).

The lentivirus group can be split into "primate" and "non-primate". Examples of primate lentiviruses include the human immunodeficiency virus (HIV), the causative agent of human acquired immunodeficiency syndrome (AIDS), and the simian immunodeficiency virus (SIV). The non-primate lentiviral group includes the prototype "slow virus" visna/maedi virus (VMV), as well as the related caprine arthritis-encephalitis virus (CAEV), equine infectious anaemia virus (EIAV) and the more recently described feline immunodeficiency virus (FIV) and bovine immunodeficiency virus (BIV).

Details on the genomic structure of some lentiviruses may be found in the art. By way of example, details on HIV and EIAV may be found from the NCBI Genbank database (i.e. Genome Accession Nos. AF033819 and AF033820 respectively). Details of HIV variants may also be found at http://hiv-web.lanl.gov. Details of EIAV variants may be found through http://www.ncbi.nlm.nih.gov.

During the process of infection, a retrovirus initially attaches to a specific cell surface receptor. On entry into the susceptible host cell, the retroviral RNA genome is then copied to DNA by the virally encoded reverse transcriptase which is carried inside the parent virus. This DNA is transported to the host cell nucleus where it subsequently integrates into the host genome. At this stage, it is typically referred to as the provirus. The provirus is stable in the host chromosome during cell division and is transcribed like other cellular genes. The provirus encodes the proteins and other factors required to make more virus, which can leave the cell by a process sometimes called "budding".

Each retroviral genome comprises genes called *gag*, *pol* and *env* which code for virion proteins and enzymes. These genes are flanked at both ends by regions called long terminal repeats (LTRs). The LTRs are responsible for proviral integration, and

transcription. They also serve as enhancer-promoter sequences. In other words, the LTRs can control the expression of the viral genes. Encapsidation of the retroviral RNAs occurs by virtue of a *psi* sequence located at the 5' end of the viral genome.

The LTRs themselves are identical sequences that can be divided into three elements, which are called U3, R and U5. U3 is derived from the sequence unique to the 3' end of the RNA. R is derived from a sequence repeated at both ends of the RNA and U5 is derived from the sequence unique to the 5'end of the RNA. The sizes of the three elements can vary considerably among different retroviruses.

For the viral genome, the site of transcription initiation is at the boundary between U3 and R in one LTR and the site of poly (A) addition (termination) is at the boundary between R and U5 in the other LTR. U3 contains most of the transcriptional control elements of the provirus, which include the promoter and multiple enhancer sequences responsive to cellular and in some cases, viral transcriptional activator proteins. Some retroviruses have any one or more of the following genes that code for proteins that are involved in the regulation of gene expression: *tat*, *rev*, *tax* and *rex*.

With regard to the structural genes *gag, pol* and *env* themselves, *gag* encodes the internal structural protein of the virus. Gag protein is proteolytically processed into the mature proteins MA (matrix), CA (capsid) and NC (nucleocapsid). The *pol* gene encodes the reverse transcriptase (RT), which contains DNA polymerase, associated RNase H and integrase (IN), which mediate replication of the genome. The *env* gene encodes the surface (SU) glycoprotein and the transmembrane (TM) protein of the virion, which form a complex that interacts specifically with cellular receptor proteins. This interaction leads ultimately to infection by fusion of the viral membrane with the cell membrane.

Retroviruses may also contain "additional" genes which code for proteins other than gag, pol and env. Examples of additional genes include in HIV, one or more of *vif, vpr, vpx, vpu, tat, rev* and *nef.* EIAV has (amongst others) the additional gene *S2*.

Proteins encoded by additional genes serve various functions, some of which may be duplicative of a function provided by a cellular protein. In EIAV, for example, *tat* acts as a transcriptional activator of the viral LTR. It binds to a stable, stem-loop RNA secondary structure referred to as TAR. Rev regulates and co-ordinates the expression of viral genes through rev-response elements (RRE). The mechanisms of action of these two proteins are thought to be broadly similar to the analogous mechanisms in the primate viruses. The function of S2 is unknown. In addition, an EIAV protein, Ttm, has been identified that is encoded by the first exon of *tat* spliced to the *env* coding sequence at the start of the transmembrane protein.

ADENOVIRUS VECTORS

In another embodiment of the present invention, an adenoviral vector system is used to transduce a target adipose tissue site.

By way of background information, the adenovirus is a double-stranded, linear DNA virus that does not go through an RNA intermediate. There are over 50 different human serotypes of adenovirus divided into 6 subgroups based on the genetic sequence homology. The natural target of adenovirus is the respiratory and gastrointestinal epithelia, generally giving rise to only mild symptoms. Serotypes 2 and 5 (with 95% sequence homology) are most commonly used in adenoviral vector systems and are normally associated with upper respiratory tract infections in the young.

Adenoviruses are nonenveloped, regular icosohedrons. A typical adenovirus comprises a 140nm encapsidated DNA virus. The icosahedral symmetry of the virus is composed of 152 capsomeres: 240 hexons and 12 pentons. The core of the particle contains the 36kb linear duplex DNA which is covalently associated at the 5' ends with the Terminal Protein (TP) which acts as a primer for DNA replication. The DNA has inverted terminal repeats (ITR) and the length of these varies with the serotype.

Entry of adenovirus into cells involves a series of distinct events. Attachment of the virus to the cell occurs via an interaction between the viral fibre (37nm) and the fibre receptors on the cell. This receptor has recently been identified for Ad2/5 serotypes and designated as CAR (Coxsackie and Adeno Receptor, Tomko *et al* (1997 Proc Natl Acad Sci 94: 3352-2258). Internalisation of the virus into the endosome via the cellular $\alpha v\beta 3$ and $\alpha v\beta 5$ integrins is mediated by and viral RGD sequence in the penton-base capsid protein (Wickham *et al.*, 1993 Cell 73: 309-319). Following internalisation, the endosome is disrupted by a process known as endosomolysis, an event which is believed to be preferentially promoted by the cellular $\alpha v\beta 5$ integrin (Wickham *et al.*, 1994 J Cell Biol 127: 257-264). In addition, there is recent evidence that the Ad5 fibre knob binds with high affinity to the MHC class 1 $\alpha 2$ domain at the surface of certain cell types including human epithelial and B lymphoblast cells (Hong *et al.*, 1997 EMBO 16: 2294-2306).

Subsequently the virus is translocated to the nucleus where activation of the early regions occurs and is shortly followed by DNA replication and activation of the late regions. Transcription, replication and packaging of the adenoviral DNA requires both host and viral functional protein machinery.

Viral gene expression can be divided into early (E) and late (L) phases. The late phase is defined by the onset of viral DNA replication. Adenovirus structural proteins are generally synthesised during the late phase. Following adenovirus infection, host cellular mRNA and protein synthesis is inhibited in cells infected with most serotypes. The adenovirus lytic cycle with adenovirus 2 and adenovirus 5 is very efficient and results in approximately 10, 000 virions per infected cell along with the synthesis of excess viral protein and DNA that is not incorporated into the virion. Early adenovirus transcription is a complicated sequence of interrelated biochemical events but it entails essentially the synthesis of viral RNAs prior to the onset of DNA replication.

The Schematic diagram presented in Figure 11 is of the adenovirus genome showing the relative direction and position of early and late gene transcription:

The organisation of the adenovirus genome is similiar in all of the adenovirus groups and specific functions are generally positioned at identical locations for each serotype studied. Early cytoplasmic messenger RNAs are complementary to four defined, noncontiguous regions on the viral DNA. These regions are designated E1-E4. The early transcripts have been classified into an array of intermediate early (E1a), delayed early (E1b, E2a, E2b, E3 and E4), and intermediate regions.

The early genes are expressed about 6-8 hours after infection and are driven from 7 promoters in gene blocks E1-4.

The E1a region is involved in transcriptional transactivation of viral and cellular genes as well as transcriptional repression of other sequences. The E1a gene exerts an important control function on all of the other early adenovirus messenger RNAs. In normal tisssues, in order to transcribe regions E1b, E2a, E2b, E3 or E4 efficiently, active E1a product is required. However, the E1a function may be bypassed. Cells may be manipulated to provide E1a-like functions or may naturally contain such functions. The virus may also be manipulated to bypass the E1a function. The viral packaging signal overlaps with the E1a enhancer (194-358 nt).

The E1b region influences viral and cellular metabolism and host protein shut-off. It also includes the gene encoding the pIX protein (3525-4088 nt) which is required for packaging of the full length viral DNA and is important for the thermostability of the virus. The E1b region is required for the normal progression of viral events late in infection. The E1b product acts in the host nucleus. Mutants generated within the E1b sequences exhibit diminished late viral mRNA accumulation as well as impairment in the inhibition of host cellular transport normally observed late in adenovirus infection. E1b is required for altering functions of the host cell such that processing and transport are shifted in favour of viral late gene products. These products then result in viral packaging and release of virions. E1b produces a 19 kD protein that prevents apoptosis. E1b also produces a 55 kD protein that binds to p53. For a review on adenoviruses and their replication, see WO 96/17053.

The E2 region is essential as it encodes the 72 kDa DNA binding protein, DNA polymerase and the 80 kDa precurser of the 55 kDa Terminal Protein (TP) needed for protein priming to initiate DNA synthesis.

A 19 kDa protein (gp19K) is encoded within the E3 region and has been implicated in modulating the host immune response to the virus. Expression of this protein is upregulated in response to TNF alpha during the first phase of the infection and this then binds and prevents migration of the MHC class I antigens to the epithelial surface, thereby dampening the recognition of the adenoviral infected cells by the cytotoxic T lymphocytes. The E3 region is dispensible in *in vitro* studies and can be removed by deletion of a 1.9 kb *Xba*I fragment.

The E4 region is concerned with decreasing the host protein synthesis and increasing the DNA replication of the virus.

There are 5 families of late genes and all are initiated from the major late promoter. The expression of the late genes includes a very complex post-transcriptional control mechanism involving RNA splicing. The fibre protein is encoded within the L5 region. The adenoviral genome is flanked by the inverted terminal repeat which in Ad5 is 103 bp and is essential for DNA replication. 30-40 hours post infection viral production is complete.

Adenoviruses may be converted for use as vectors for gene transfer by deleting the E1 gene, which is important for the induction of the E2, E3 and E4 promoters. The E1-replication defective virus may be propagated in a cell line that provides the E1 polypeptides in trans, such as the human embryonic kidney cell line 293. A therapeutic gene or genes can be inserted by recombination in place of the E1 gene. Expression of the gene is driven from either the E1 promoter or a heterologous promoter.

Even more attenuated adenoviral vectors have been developed by deleting some or all of the E4 open reading frames (ORFs). However, certain second generation vectors appear not to give longer-term gene expression, even though the DNA seems to be

maintained. Thus, it appears that the function of one or more of the E4 ORFs may be to enhance gene expression from at least certain viral promoters carried by the virus.

An alternative approach to making a more defective virus has been to "gut" the virus completely maintaining only the terminal repeats required for viral replication. The "gutted" or "gutless" viruses can be grown to high titres with a first generation helper virus in the 293 cell line but it has been difficult to separate the "gutted" vector from the helper virus.

The adenovirus provides advantages as a vector for gene delivery.

It is a double stranded DNA nonenveloped virus that is capable of *in vivo* and *in vitro* transduction of a broad range of cell types of human and non-human origin. These cells include respiratory airway epithelial cells, hepatocytes, muscle cells, cardiac myocytes, synoviocytes, primary mammary epithelial cells and post-mitotically terminally differentiated cells such as neurons.

Adenoviral vectors are also capable of transducing non dividing cells. This is very important for diseases, such as cystic fibrosis, in which the affected cells in the lung epithelium, have a slow turnover rate. In fact, several trials are underway utilising adenovirus-mediated transfer of cystic fibrosis transporter (CFTR) into the lungs of afflicted adult cystic fibrosis patients.

Adenoviruses have been used as vectors for gene therapy and for expression of heterologous genes. The large (36 kilobase) genome can accommodate up to 8kb of foreign insert DNA and is able to replicate efficiently in complementing cell lines to produce very high titres of up to 10^{12}. Adenovirus is thus one of the best systems to study the expression of genes in primary non-replicative cells.

The expression of viral or foreign genes from the adenovirus genome does not require a replicating cell. Adenoviral vectors enter cells by receptor mediated endocytosis. Once inside the cell, adenovirus vectors rarely integrate into the host chromosome. Instead, it functions episomally (independently from the host genome) as a linear

genome in the host nucleus. Hence the use of recombinant adenovirus alleviates the problems associated with random integration into the host genome.

In one embodiment of the present invention, the features of adenoviruses may be combined with the genetic stability of lentiviruses which can be used to transduce target adipose tissue cells to become transient lentiviral producer cells capable of stably infect neighbouring cells. Such lentiviral producer cells which are engineered to express an NOI of the present invention can be implanted in organisms such as animals or humans for use in the treatment of disease such as cancer. Adenoviral delivery systems have been described in WO 00/17371.

POX VIRUSES

In a further embodiment of the present invention, a poxviral vector system is used to transduce an adipose tissue site.

Pox viral vectors may be used in accordance with the present invention, as large fragments of DNA are easily cloned into its genome and recombinant attenuated vaccinia variants have been described (Meyer, *et al.*, 1991, J. Gen. Virol. 72: 1031-1038, Smith and Moss 1983 Gene, 25:21-28). Pox viral vector delivery systems have been described in WO 00/29428.

Examples of pox viral vectors include but are not limited to leporipoxvirus: Upton, *et al* J. Virology 60:920 (1986) (shope fibroma virus); capripoxvirus: Gershon, *et al* J. Gen. Virol. 70:525 (1989) (Kenya sheep-1); orthopoxvirus: Weir, *et al* J. Virol 46:530 (1983) (vaccinia); Esposito, *et al* Virology 135:561 (1984) (monkeypox and variola virus); Hruby, *et al* *PNAS*, 80:3411 (1983) (vaccinia); Kilpatrick, *et al* Virology 143:399 (1985) (Yaba monkey tumour virus); avipoxvirus: Binns, *et al* J. Gen. Virol 69:1275 (1988) (fowlpox); Boyle, *et al* Virology 156:355 (1987) (fowlpox); Schnitzlein, *et al* J. Virological Method, 20:341 (1988) (fowlpox, quailpox); entomopox (Lytvyn, *et al* J. Gen. Virol 73:3235-3240 (1992)].

Poxvirus vectors are used extensively as expression vehicles for genes of interest in eukaryotic cells. Their ease of cloning and propagation in a variety of host cells has led, in particular, to the widespread use of poxvirus vectors for expression of foreign protein and as delivery vehicles for vaccine antigens (Moss, B. 1991, Science 252: 1662-7).

Preferred vectors for use in accordance with the present invention are recombinant pox viral vectors such as fowl pox virus (FPV), entomopox virus, vaccinia virus such as NYVAC, canarypox virus, MVA or other non-replicating viral vector systems such as those described for example in WO 95/30018. Pox virus vectors have also been described where at least one immune evasion gene has been deleted (see WO 00/29428).

In one preferred embodiment, the pox virus vector is an entomopox virus vector.

VACCINIA VIRAL VECTORS

Preferaly the pox viral vector is a vaccinia viral vector.

Preferably, the vector is a vaccinia virus vector such as MVA or NYVAC. Most preferred is the vaccinia strain modified virus ankara (MVA) or a strain derived therefrom. Alternatives to vaccinia vectors include avipox vectors such as fowlpox or canarypox known as ALVAC and strains derived therefrom which can infect and express recombinant proteins in human cells but are unable to replicate.

Preferred vectors for use in accordance with the present invention are recombinant pox viral vectors such as fowl pox virus (FPV), entomopox virus, vaccinia virus such as NYVAC, canarypox virus, MVA or other non-replicating viral vector systems such as those described for example in WO 95/30018.

VECTOR SYSTEMS

Retroviral vector systems, such as lentiviral vector systems have been proposed as a delivery system for *inter alia* the transfer of a NOI to one or more sites of interest. The transfer can occur *in vitro*, *ex vivo*, *in vivo,* or combinations thereof. Retroviral vector systems have even been exploited to study various aspects of the retrovirus life cycle, including receptor usage, reverse transcription and RNA packaging (reviewed by Miller, 1992 Curr Top Microbiol Immunol 158:1-24).

As used herein the term "vector system" means a vector particle capable of transducing a recipient cell with an NOI.

A vector particle includes the following components: a vector genome, which may contain one or more NOIs, a nucleocapsid encapsidating the nucleic acid, and a membrane surrounding the nucleocapsid.

The term "nucleocapsid" refers to at least the group specific viral core proteins (gag) and the viral polymerase (pol) of a retrovirus genome. These proteins encapsidate the packagable sequences and are themselves further surrounded by a membrane containing an envelope glycoprotein.

Once within the cell, the RNA genome from a retroviral vector particle is reverse transcribed into DNA and integrated into the DNA of the recipient cell.

The term "vector genome" refers to both to the RNA construct present in the retroviral vector particle and the integrated DNA construct. The term also embraces a separate or isolated DNA construct capable of encoding such an RNA genome. A retroviral or lentiviral genome should comprise at least one component part derivable from a retrovirus or a lentivirus. The term "derivable" is used in its normal sense as meaning a nucleotide sequence or a part thereof which need not necessarily be obtained from a retrovirus such as a lentivirus but instead could be derived therefrom. By way of example, the sequence may be prepared synthetically or by use of

recombinant DNA techniques. Preferably the genome comprises a *psi* region (or an analogous component which is capable of causing encapsidation).

The viral vector genome is preferably "replication defective" by which we mean that the genome does not comprise sufficient genetic information alone to enable independent replication to produce infectious viral particles within the recipient cell. In a preferred embodiment, the genome lacks a functional *env, gag* or *pol* gene. If a highly preferred embodiment the genome lacks *env, gag* and *pol* genes.

The viral vector genome may comprise some or all of the long terminal repeats (LTRs). Preferably the genome comprises at least part of the LTRs or an analogous sequence which is capable of mediating proviral integration, and transcription. The sequence may also comprise or act as an enhancer-promoter sequence.

It is known that the separate expression of the components required to produce a retroviral vector particle on separate DNA sequences cointroduced into the same cell will yield retroviral particles carrying defective retroviral genomes that carry therapeutic genes (e.g. Reviewed by Miller 1992). This cell is referred to as the producer cell (see below).

There are two common procedures for generating producer cells. In one, the sequences encoding retroviral Gag, Pol and Env proteins are introduced into the cell and stably integrated into the cell genome; a stable cell line is produced which is referred to as the packaging cell line. The packaging cell line produces the proteins required for packaging retroviral RNA but it cannot bring about encapsidation due to the lack of a *psi* region. However, when a vector genome (having a *psi* region) is introduced into the packaging cell line, the helper proteins can package the *psi*-positive recombinant vector RNA to produce the recombinant virus stock. This can be used to transduce the NOI into recipient cells. The recombinant virus whose genome lacks all genes required to make viral proteins can infect only once and cannot propagate. Hence, the NOI is introduced into the host cell genome without the generation of potentially harmful retrovirus. A summary of the available packaging lines is presented in

"Retroviruses" (1997 Cold Spring Harbour Laboratory Press Eds: JM Coffin, SM Hughes, HE Varmus pp 449).

The present invention also provides a packaging cell line comprising a viral vector genome which is capable of producing a vector system useful in the first aspect of the invention. For example, the packaging cell line may be transduced with a viral vector system comprising the genome or transfected with a plasmid carrying a DNA construct capable of encoding the RNA genome. The present invention also provides a kit for producing a viral vector system useful in the first aspect of the invention which comprises a packaging cell and a viral vector genome.

The second approach is to introduce the three different DNA sequences that are required to produce a viral vector particle, such as a lentiviral vector partile i.e. the *env* coding sequences, the *gag-pol* coding sequence and the defective lentiviral genome containing one or more NOIs into the cell at the same time by transient transfection and the procedure is referred to as transient triple transfection (Landau & Littman 1992; Pear et al 1993). The triple transfection procedure has been optimised (Soneoka et al 1995; Finer et al 1994). WO 94/29438 describes the production of producer cells *in vitro* using this multiple DNA transient transfection method. WO 97/27310 describes a set of DNA sequences for creating lentiviral producer cells either *in vivo* or *in vitro* for re-implantation.

Transient transfection has numerous advantages over the packaging cell method. In this regard, transient transfection avoids the longer time required to generate stable vector-producing cell lines and is used if the vector genome or retroviral packaging components are toxic to cells. If the vector genome encodes toxic genes or genes that interfere with the replication of the host cell, such as inhibitors of the cell cycle or genes that induce apoptosis, it may be difficult to generate stable vector-producing cell lines, but transient transfection can be used to produce the vector before the cells die. Also, cell lines have been developed using transient infection that produce vector titre levels that are comparable to the levels obtained from stable vector-producing cell lines (Pear et al 1993, PNAS 90:8392-8396).

The components of the viral system which are required to complement the vector genome may be present on one or more "producer plasmids" for transfecting into cells.

The present invention also provides a kit for producing a viral vector system useful in the first aspect of the invention, comprising

(i) a viral vector genome which is incapable of encoding one or more proteins which are required to produce a vector particle;

(ii) one or more producer plasmid(s) capable of encoding the protein which is not encoded by (i); and optionally

(iii) a cell suitable for conversion into a producer cell.

In a preferred embodiment, the viral vector genome is incapable of encoding the proteins gag, pol and env. Preferably the kit comprises one or more producer plasmids encoding env, gag and pol, for example, one producer plasmid encoding env and one encoding gag-pol. Preferably the gag-pol sequence is codon optimised for use in the particular producer cell (see below).

The present invention also provides a producer cell expressing the vector genome and the producer plasmid(s) capable of producing a viral vector system useful in the present invention.

Preferably the viral vector system used in the first aspect of the present invention is a self-inactivating (SIN) vector system.

By way of example, self-inactivating retroviral vector systems have been constructed by deleting the transcriptional enhancers or the enhancers and promoter in the U3 region of the 3′ LTR. After a round of vector reverse transcription and integration, these changes are copied into both the 5′ and the 3′ LTRs producing a transcriptionally inactive provirus . However, any promoter(s) internal to the LTRs in such vectors will still be transcriptionally active. This strategy has been employed to eliminate effects of the enhancers and promoters in the viral LTRs on transcription from internally placed genes. Such effects include increased transcription or suppression of transcription. This strategy can also be used to eliminate downstream

transcription from the 3′ LTR into genomic DNA. This is of particular concern in human gene therapy where it may be important to prevent the adventitious activation of an endogenous oncogene.

Preferably a recombinase assisted mechanism is used which facilitates the production of high titre regulated lentiviral vectors from the producer cells of the present invention.

As used herein, the term "recombinase assisted system" includes but is not limited to a system using the Cre recombinase / loxP recognition sites of bacteriophage P1 or the site-specific FLP recombinase of *S. cerevisiae* which catalyses recombination events between 34 bp FLP recognition targets (FRTs).

The site-specific FLP recombinase of *S. cerevisiae* which catalyses recombination events between 34 bp FLP recognition targets (FRTs) has been configured into DNA constructs in order to generate high level producer cell lines using recombinase-assisted recombination events (Karreman et al (1996) NAR 24:1616-1624). A similar system has been developed using the Cre recombinase / loxP recognition sites of bacteriophage P1 (see PCT/GB00/03837; Vanin et al (1997) J. Virol 71:7820-7826). This was configured into a lentiviral genome such that high titre lentiviral producer cell lines were generated.

By using producer/packaging cell lines, it is possible to propagate and isolate quantities of viral vector particles (e.g. to prepare suitable titres of the viral vector particles) for subsequent transduction of, for example, a site of interest (such as adult brain tissue). Producer cell lines are usually better for large scale production or vector particles.

Producer cells/packaging cells can be of any suitable cell type. Producer cells are generally mammalian cells but can be, for example, insect cells.

As used herein, the term "producer cell" or "vector producing cell" refers to a cell which contains all the elements necessary for production of retroviral vector particles. Preferably, the producer cell is obtainable from a stable producer cell line.

Preferably, the producer cell is obtainable from a derived stable producer cell line.

Preferably, the producer cell is obtainable from a derived producer cell line.

As used herein, the term "derived producer cell line" is a transduced producer cell line which has been screened and selected for high expression of a marker gene. Such cell lines support high level expression from the viral genome. The term "derived producer cell line" is used interchangeably with the term "derived stable producer cell line" and the term "stable producer cell line.

Preferably the derived producer cell line includes but is not limited to a retroviral and/or a lentiviral producer cell.

Preferably the derived producer cell line is an HIV or EIAV producer cell line, more preferably an EIAV producer cell line.

Preferably the envelope protein sequences, and nucleocapsid sequences are all stably integrated in the producer and/or packaging cell. However, one or more of these sequences could also exist in episomal form and gene expression could occur from the episome.

As used herein, the term "packaging cell" refers to a cell which contains those elements necessary for production of infectious recombinant virus which are lacking in the RNA genome. Typically, such packaging cells contain one or more producer plasmids which are capable of expressing viral structural proteins (such as *gag-pol* and *env,* which may be codon optimised) but they do not contain a packaging signal.

The term "packaging signal" which is referred to interchangeably as "packaging sequence" or "*psi*" is used in reference to the non-coding, *cis*-acting sequence required for encapsidation of retroviral RNA strands during viral particle formation. In HIV-1, this sequence has been mapped to loci extending from upstream of the major splice donor site (SD) to at least the *gag* start codon.

Packaging cell lines may be readily prepared (see also WO 92/05266), and utilised to create producer cell lines for the production of retroviral vector particles. As already mentioned above, a summary of the available packaging lines is presented in "Retroviruses".

Also as discussed above, simple packaging cell lines, comprising a provirus in which the packaging signal has been deleted, have been found to lead to the rapid production of undesirable replication competent viruses through recombination. In order to improve safety, second generation cell lines have been produced wherein the 3'LTR of the provirus is deleted. In such cells, two recombinations would be necessary to produce a wild type virus. A further improvement involves the introduction of the *gag-pol* genes and the *env* gene on separate constructs so-called third generation packaging cell lines. These constructs are introduced sequentially to prevent recombination during transfection.

Preferably, the packaging cell lines are second generation packaging cell lines.

Preferably, the packaging cell lines are third generation packaging cell lines.

In these split-construct, third generation cell lines, a further reduction in recombination may be achieved by changing the codons. This technique, based on the redundancy of the genetic code, aims to reduce homology between the separate constructs, for example between the regions of overlap in the *gag-pol* and *env* open reading frames.

The packaging cell lines are useful for providing the gene products necessary to encapsidate and provide a membrane protein for a high titre vector particle production. The packaging cell may be a cell cultured *in vitro* such as a tissue culture cell line. Suitable cell lines include but are not limited to mammalian cells such as murine fibroblast derived cell lines or human cell lines. Preferably the packaging cell line is a human cell line, such as for example: HEK293, 293-T, TE671, HT1080.

Alternatively, the packaging cell may be a cell derived from the individual to be treated such as a monocyte, macrophage, blood cell or fibroblast. The cell may be isolated from an individual and the packaging and vector components administered *ex vivo* followed by re-administration of the autologous packaging cells.

It is highly desirable to use high-titre virus preparations in both experimental and practical applications. Techniques for increasing viral titre include using a *psi* plus packaging signal as discussed above and concentration of viral stocks.

As used herein, the term "high titre" means an effective amount of a viral vector or particle which is capable of transducing a target site such as a target adipose tissue site.

As used herein, the term "effective amount" means an amount of a regulated viral or lentiviral vector or vector particle which is sufficient to induce expression of the NOIs at a target adipose tissue site.

A high-titre viral preparation for a producer/packaging cell is usually of the order of 10^5 to 10^7 t.u. per ml. (The titer is expressed in transducing units per ml (t.u./ml) as titred on a standard D17 cell line). For transduction in adipose tissues, it may be necessary to use very small volumes, so the viral preparation is concentrated by ultracentrifugation. The resulting preparation should have at least 10^8 t.u./ml, preferably from 10^8 to 10^9 t.u./ml, more preferably at least 10^9 t.u./ml.

The expression products encoded by the NOIs may be proteins which are secreted from the cell. Alternatively the NOI expression products are not secreted and are active within the cell. For some applications, it is preferred for the NOI expression product to demonstrate a bystander effect or a distant bystander effect; that is the production of the expression product in one cell leading to the modulation of additional, related cells, either neighbouring or distant (e.g. metastatic), which possess a common phenotype.

The presence of a sequence termed the central polypurine tract (cPPT) may improve the efficiency of gene delivery to non-dividing cells (see WO 00/31200). This *cis*-acting element is located, for example, in the EIAV polymerase coding region element. Preferably the genome of the vector system used in the present invention comprises a cPPT sequence. In addition, or in the alternative, the viral genome may comprise a post-translational regulatory element and/or a translational enhancer.

The NOIs may be operatively linked to one or more promoter/enhancer elements. Transcription of one or more NOI may be under the control of viral LTRs or alternatively promoter-enhancer elements can be engineered in with the transgene. Preferably the promoter is a strong promoter such as CMV. The promoter may be a regulated promoter. The promoter may be tissue-specific.

MINIMAL SYSTEMS

It has been demonstrated that a primate lentivirus minimal system can be constructed which requires none of the HIV/SIV additional genes *vif, vpr, vpx, vpu, tat, rev* and *nef* for either vector production or for transduction of dividing and non-dividing cells. It has also been demonstrated that an EIAV minimal vector system can be constructed which does not require *S2* for either vector production or for transduction of dividing and non-dividing cells. The deletion of additional genes is highly advantageous. Firstly, it permits vectors to be produced without the genes associated with disease in lentiviral (e.g. HIV) infections. In particular, *tat* is associated with disease. Secondly, the deletion of additional genes permits the vector to package more heterologous DNA. Thirdly, genes whose function is unknown, such as *S2*, may be omitted, thus reducing the risk of causing undesired effects. Examples of minimal lentiviral vectors are disclosed in WO-A-99/32646 and in WO-A-98/17815.

Thus, preferably, the delivery system used in the invention is devoid of at least *tat* and *S2* (if it is an EIAV vector system), and possibly also *vif, vpr, vpx, vpu* and *nef.* More preferably, the systems of the present invention are also devoid of *rev*. Rev was previously thought to be essential in some retroviral genomes for efficient virus production. For example, in the case of HIV, it was thought that *rev* and RRE

sequence should be included. However, it has been found that the requirement for *rev* and RRE can be reduced or eliminated by codon optimisation (see below) or by replacement with other functional equivalent systems such as the MPMV system. As expression of the codon optimised *gag-pol* is REV independent, RRE can be removed from the *gag-pol* expression cassette, thus removing any potential for recombination with any RRE contained on the vector genome.

In a preferred embodiment the viral genome of the first aspect of the invention lacks the Rev response element (RRE).

In a preferred embodiment, the system used in the present invention is based on a so-called "minimal" system in which some or all of the additional genes have be removed.

CODON OPTIMISATION

Codon optimisation has previously been described in WO99/41397. Different cells differ it their usage of particular codons. This codon bias corresponds to a bias in the relative abundance of particular tRNAs in the cell type. By altering the codons in the sequence so that they are tailored to match with the relative abundance of corresponding tRNAs, it is possible to increase expression. By the same token, it is possible to decrease expression by deliberately choosing codons for which the corrsponding tRNAs are known to be rare in the particular cell type. Thus, an additional degree of translational control is available.

Many viruses, including HIV and other lentiviruses, use a large number of rare codons and by changing these to correspond to commonly used mammalian codons, increased expression of the packaging components in mammalian producer cells can be achieved. Codon usage tables are known in the art for mammalian cells, as well as for a variety of other organisms.

Codon optimisation has a number of other advantages. By virtue of alterations in their sequences, the nucleotide sequences encoding the packaging components of the

viral particles required for assembly of viral particles in the producer cells/packaging cells have RNA instability sequences (INS) eliminated from them. At the same time, the amino acid sequence coding sequence for the packaging components is retained so that the viral components encoded by the sequences remain the same, or at least sufficiently similar that the function of the packaging components is not compromised. Codon optimisation also overcomes the Rev/RRE requirement for export, rendering optimised sequences Rev independent. Codon optimisation also reduces homologous recombination between different constructs within the vector system (for example between the regions of overlap in the gag-pol and env open reading frames). The overall effect of codon optimisation is therefore a notable increase in viral titre and improved safety.

In one embodiment only codons relating to INS are codon optimised. However, in a much more preferred and practical embodiment, the sequences are codon optimised in their entirety, with the exception of the sequence encompassing the frameshift site.

The *gag-pol* gene comprises two overlapping reading frames encoding the gag-pol proteins. The expression of both proteins depends on a frameshift during translation. This frameshift occurs as a result of ribosome "slippage" during translation. This slippage is thought to be caused at least in part by ribosome-stalling RNA secondary structures. Such secondary structures exist downstream of the frameshift site in the *gag-pol* gene. For HIV, the region of overlap extends from nucleotide 1222 downstream of the beginning of *gag* (wherein nucleotide 1 is the A of the *gag* ATG) to the end of *gag* (nt 1503). Consequently, a 281 bp fragment spanning the frameshift site and the overlapping region of the two reading frames is preferably not codon optimised. Retaining this fragment will enable more efficient expression of the gag-pol proteins.

For EIAV the beginning of the overlap has been taken to be nt 1262 (where nucleotide 1 is the A of the *gag* ATG). The end of the overlap is at 1461 bp. In order to ensure that the frameshift site and the *gag-pol* overlap are preserved, the wild type sequence has been retained from nt 1156 to 1465.

Derivations from optimal codon usage may be made, for example, in order to accommodate convenient restriction sites, and conservative amino acid changes may be introduced into the gag-pol proteins.

In a highly preferred embodiment, codon optimisation was based on lightly expressed mammalian genes. The third and sometimes the second and third base may be changed.

Due to the degenerate nature of the Genetic Code, it will be appreciated that numerous *gag-pol* sequences can be achieved by a skilled worker. Also there are many retroviral variants described which can be used as a starting point for generating a codon optimised *gag-pol* sequence. Lentiviral genomes can be quite variable. For example there are many quasi-species of HIV-1 which are still functional. This is also the case for EIAV. These variants may be used to enhance particular parts of the transduction process. Examples of HIV-1 variants may be found at http://hiv-web.lanl.gov. Details of EIAV clones may be found at the NCBI database: http://www.ncbi.nlm.nih.gov.

The strategy for codon optimised *gag-pol* sequences can be used in relation to any retrovirus. This would apply to all lentiviruses, including EIAV, FIV, BIV, CAEV, VMR, SIV, HIV-1 and HIV-2. In addition this method could be used to increase expression of genes from HTLV-1, HTLV-2, HFV, HSRV and human endogenous retroviruses (HERV), MLV and other retroviruses.

Codon optimisation can render *gag-pol* expression Rev independent. In order to enable the use of anti-*rev* or RRE factors in the retroviral vector, however, it would be necessary to render the viral vector generation system totally Rev/RRE independent. Thus, the genome also needs to be modified. This is achieved by optimising vector genome components. Advantageously, these modifications also lead to the production of a safer system absent of all additional proteins both in the producer and in the transduced cell.

As described above, the packaging components for a retroviral vector include expression products of *gag, pol* and *env* genes. In addition, efficient packaging depends on a short sequence of 4 stem loops followed by a partial sequence from *gag* and *env* (the "packaging signal"). Thus, inclusion of a deleted *gag* sequence in the retroviral vector genome (in addition to the full *gag* sequence on the packaging construct) will optimise vector titre. To date efficient packaging has been reported to require from 255 to 360 nucleotides of *gag* in vectors that still retain *env* sequences, or about 40 nucleotides of *gag* in a particular combination of splice donor mutation, *gag* and *env* deletions. It has surprisingly been found that a deletion of all but the N-termnial 360 or so nucleotides in *gag* leads to an increase in vector titre. Thus, preferably, the retroviral vector genome includes a *gag* sequence which comprises one or more deletions, more preferably the gag sequence comprises about 360 nucleotides derivable from the N-terminus.

PSEUDOTYPING

In the design of viral vector systems, such as lentiviral vector systems, it is desirable to engineer particles with different target cell specificities to the native virus, to enable the delivery of genetic material to an expanded or altered range of cell types. One manner in which to achieve this is by engineering the virus envelope protein to alter its specificity. Another approach is to introduce a heterologous envelope protein into the vector particle to replace or add to the native envelope protein of the virus.

The term pseudotyping means incorporating in at least a part of, or substituting a part of, or replacing all of, an *env* gene of a viral genome with a heterologous *env* gene, for example an *env* gene from another virus. Pseudotyping is not a new phenomenon and examples may be found in WO 99/61639, WO-A-98/05759, WO-A-98/05754, WO-A-97/17457, WO-A-96/09400, WO-A-91/00047 and Mebatsion *et al* 1997 Cell 90, 841-847.

Pseudotyping can improve retroviral vector stability and transduction efficiency. A pseudotype of murine leukemia virus packaged with lymphocytic choriomeningitis virus (LCMV) has been described (Miletic et al (1999) J. Virol. 73:6114-6116) and

shown to be stable during ultracentrifugation and capable of infecting several cell lines from different species. Other envelope proteins, such as envelope proteins from the Ebola virus may also be used.

In one embodiment of the present invention, the vector system may be pseudotyped with LMCV env protein.

In another embodiment of the present invention, the vector system may be pseudotyped with an envelope proteins from the Ebola virus.

In another embodiment of the present invention the viral vector system may be pseudotyped with at least a part of a rabies G protein or a mutant, variant, homologue or fragment thereof, or at least a part of a VSV G protein or a mutant, variant, homologue or fragment thereof.

Thus, in one embodiment of the present invention, there is provided the use of a viral delivery system comprising a heterologous *env* region, wherein the heterologous *env* region comprises at least a part of a rabies G protein or a mutant, variant, homologue or fragment thereof, or at least a part of a VSV G protein or a mutant, variant, homologue or fragment thereof to transduce a target adipose tissue site.

The heterologous env region may be encoded by a gene which is present on a producer plasmid. The producer plasmid may be present as part of a kit for the production of viral vector particles suitable for use in the first aspect of the invention.

RABIES G PROTEIN

In another embodiment of the present invention, the vector system may be pseudotyped with at least a part of a rabies G protein or a mutant, variant, homologue or fragment thereof.

Teachings on the rabies G protein, as well as mutants thereof, may be found in in WO 99/61639 and well as Rose *et al.*, 1982 J. Virol. 43: 361-364, Hanham *et al.,* 1993 J.

Virol.,67, 530-542, Tuffereau *et al.*,1998 J. Virol., 72, 1085-1091, Kucera *et al.*, 1985 J. Virol 55, 158-162, Dietzschold *et al.*, 1983 PNAS 80, 70-74, Seif *et al.*, 1985 J.Virol., 53, 926-934, Coulon *et al.*,1998 J. Virol., 72, 273-278, Tuffereau *et al.*,1998 J. Virol., 72, 1085-10910, Burger *et al.*, 1991 J.Gen. Virol. 72. 359-367, Gaudin *et al* 1995 J Virol 69, 5528-5534, Benmansour *et al* 1991 J Virol 65, 4198-4203, Luo *et al* 1998 Microbiol Immunol 42, 187-193, Coll 1997 Arch Virol 142, 2089-2097, Luo *et al* 1997 Virus Res 51, 35-41, Luo *et al* 1998 Microbiol Immunol 42, 187-193, Coll 1995 Arch Virol 140, 827-851, Tuchiya *et al* 1992 Virus Res 25, 1-13, Morimoto *et al* 1992 Virology 189, 203-216, Gaudin *et al* 1992 Virology 187, 627-632, Whitt *et al* 1991 Virology 185, 681-688, Dietzschold *et al* 1978 J Gen Virol 40, 131-139, Dietzschold *et al* 1978 Dev Biol Stand 40, 45-55, Dietzschold *et al* 1977 J Virol 23, 286-293, and Otvos *et al* 1994 Biochim Biophys Acta 1224, 68-76. A rabies G protein is also described in EP-A-0445625.

The use of rabies G protein provides vectors which, *in vivo,* preferentially transduce targeted cells which rabies virus preferentially infects. This includes adipose tissue target cells *in vivo*. For an adipose tissue targeted vector, rabies G from a pathogenic strain of rabies such as ERA may be particularly effective. On the other hand rabies G protein confers a wider target cell range *in vitro* including nearly all mammalian and avian cell types tested (Seganti *et al.*, 1990 Arch Virol. 34,155-163; Fields *et al.*, 1996 Fields Virology, Third Edition, vol.2, Lippincott-Raven Publishers, Philadelphia, New York).

The tropism of the pseudotyped vector particles may be modified by the use of a mutant rabies G which is modified in the extracellular domain. Rabies G protein has the advantage of being mutatable to restrict target cell range. The uptake of rabies virus by target cells *in vivo* is thought to be mediated by the acetylcholine receptor (AchR) but there may be other receptors to which in binds *in vivo* (Hanham *et al.*, 1993 J. Virol.,67, 530-542; Tuffereau *et al.*,1998 J. Virol., 72, 1085-1091). It is thought that multiple receptors are used in the nervous system for viral entry, including NCAM (Thoulouze et al (1998) J. Virol 72(9):7181-90) and p75 Neurotrophin receptor (Tuffereau C et al (1998) Embo J 17(24) 7250-9).

The effects of mutations in antigenic site III of the rabies G protein on virus tropism have been investigated, this region is not thought to be involved in the binding of the virus to the acetylcholine receptor (Kucera *et al.*, 1985 J. Virol 55, 158-162; Dietzschold *et al.*, 1983 Proc Natl Acad Sci 80, 70-74; Seif *et al.*, 1985 J.Virol., 53, 926-934; Coulon *et al.*,1998 J. Virol., 72, 273-278; Tuffereau *et al.*,1998 J. Virol., 72, 1085-10910). For example a mutation of the arginine at amino acid 333 in the mature protein to glutamine can be used to restrict viral entry to olfactory and peripheral neurons *in vivo* while reducing propagation to the central nervous system. These viruses were able to penetrate motor neurons and sensory neurons as efficiently as the wild type virus, yet transneuronal transfer did not occur (Coulon *et al.*, 1989; J. Virol. 63, 3550-3554). Viruses in which amino acid 330 has been mutated are further attenuated, being unable to infect either motor neurons or sensory neurons after intra-muscular injection (Coulon *et al.*,1998 J. Virol., 72, 273-278).

Alternatively or additionally, rabies G proteins from laboratory passaged strains of rabies may be used. These can be screened for alterations in tropism. Such strains include the following:

Genbank accession number	Rabies Strain
J02293	ERA
U52947	COSRV
U27214	NY 516
U27215	NY771
U27216	FLA125
U52946	SHBRV
M32751	HEP-Flury

By way of example, the ERA strain is a pathogenic strain of rabies and the rabies G protein from this strain can be used for transduction of neuronal cells. The sequence of rabies G from the ERA strains is in the GenBank database (accession number J02293). This protein has a signal peptide of 19 amino acids and the mature protein

begins at the lysine residue 20 amino acids from the translation initiation methionine. The HEP-Flury strain contains the mutation from arginine to glutamine at amino acid position 333 in the mature protein which correlates with reduced pathogenicity and which can be used to restrict the tropism of the viral envelope.

WO 99/61639 discloses the nucleic and amino acid sequences for a rabies virus strain ERA (Genbank locus RAVGPLS, accession M38452).

VSV-G PROTEIN

The envelope glycoprotein (G) of Vesicular stomatitis virus (VSV), a rhabdovirus, is another envelope protein that has been shown to be capable of pseudotyping certain retroviruses.

Its ability to pseudotype MoMLV- based retroviral vectors in the absence of any retroviral envelope proteins was first shown by Emi *et al* (1991 Journal of Virology 65:1202-1207). WO94/294440 teaches that retroviral vectors may be successfully pseudotyped with VSV-G. These pseudotyped VSV-G vectors may be used to transduce a wide range of mammalian cells. Even more recently, Abe et al (J Virol 1998 72(8) 6356-6361) teach that non-infectious retroviral particles can be made infectious by the addition of VSV-G.

Burns *et al* (1993 Proc. Natl. Acad. Sci. USA 90: 8033-7) successfully pseudotyped the retrovirus MLV with VSV-G and this resulted in a vector having an altered host range compared to MLV in its native form. VSV-G pseudotyped vectors have been shown to infect not only mammalian cells, but also cell lines derived from fish, reptiles and insects (Burns *et al* 1993 *ibid*). They have also been shown to be more efficient than traditional amphotropic envelopes for a variety of cell lines (Yee *et al*, 1994 Proc. Natl. Acad. Sci. USA 91: 9564-9568, Lin, Emi *et al*, 1991 Journal of Virology 65:1202-1207). VSV-G protein can be used to pseudotype certain retroviruses because its cytoplasmic tail is capable of interacting with the retroviral cores.

The provision of a non-retroviral pseudotyping envelope such as VSV-G protein gives the advantage that vector particles can be concentrated to a high titre without loss of infectivity (Akkina *et al*, 1996 J. Virol. 70: 2581-5). Retrovirus envelope proteins are apparently unable to withstand the shearing forces during ultracentrifugation, probably because they consist of two non-covalently linked subunits. The interaction between the subunits may be disrupted by the centrifugation. In comparison the VSV glycoprotein is composed of a single unit. VSV-G protein pseudotyping can therefore offer potential advantages.

WO 00/52188 describes the generation of pseudotyped retroviral vectors, from stable producer cell lines, having vesicular stomatitis virus-G protein (VSV-G) as the membrane-associated viral envelope protein, and provides a gene sequence for the VSV-G protein.

MUTANTS, VARIANTS, HOMOLOGUES AND FRAGMENTS

In one embodiment of the present invention, the viral vector system used in the present invention may be pseudotyped with a mutant, variant, homologue or fragment of the wild-type Rabies G or VSV-G protein.

The term "wild type" is used to mean an polypeptide having a primary amino acid sequence which is identical with the native protein (i.e., the viral protein).

The term "mutant" is used to mean a polypeptide having a primary amino acid sequence which differs from the wild type sequence by one or more amino acid additions, substitutions or deletions. A mutant may arise naturally, or may be created artificially (for example by site-directed mutagenesis).Preferably the mutant has at least 90% sequence identity with the wild type sequence. Preferably the mutant has 20 mutations or less over the whole wild-type sequence. More preferably the mutant has 10 mutations or less, most preferably 5 mutations or less over the whole wild-type sequence.

The term "variant" is used to mean a naturally occurring polypeptide which differs from a wild-type sequence. A variant may be found within the same viral strain (i.e. if there is more than one isoform of the protein) or may be found within a different strains. Preferably the variant has at least 90% sequence identity with the wild type sequence. Preferably the variant has 20 mutations or less over the whole wild-type sequence. More preferably the variant has 10 mutations or less, most preferably 5 mutations or less over the whole wild-type sequence.

Here, the term "homologue" means an entity having a certain homology with the wild type amino acid sequence and the wild type nucleotide sequence. Here, the term "homology" can be equated with "identity".

In the present context, an homologous sequence is taken to include an amino acid sequence which may be at least 75, 85 or 90% identical, preferably at least 95 or 98% identical to the subject sequence. Typically, the homologues will comprise the same active sites etc. as the subject amino acid sequence. Although homology can also be considered in terms of similarity (i.e. amino acid residues having similar chemical properties/functions), in the context of the present invention it is preferred to express homology in terms of sequence identity.

In the present context, an homologous sequence is taken to include a nucleotide sequence which may be at least 75, 85 or 90% identical, preferably at least 95 or 98% identical to the subject sequence. Typically, the homologues will comprise the same sequences that code for the active sites etc. as the subject sequence. Although homology can also be considered in terms of similarity (i.e. amino acid residues having similar chemical properties/functions), in the context of the present invention it is preferred to express homology in terms of sequence identity.

Homology comparisons can be conducted by eye, or more usually, with the aid of readily available sequence comparison programs. These commercially available computer programs can calculate % homology between two or more sequences.

% homology may be calculated over contiguous sequences, i.e. one sequence is aligned with the other sequence and each amino acid in one sequence is directly compared with the corresponding amino acid in the other sequence, one residue at a time. This is called an "ungapped" alignment. Typically, such ungapped alignments are performed only over a relatively short number of residues.

Although this is a very simple and consistent method, it fails to take into consideration that, for example, in an otherwise identical pair of sequences, one insertion or deletion will cause the following amino acid residues to be put out of alignment, thus potentially resulting in a large reduction in % homology when a global alignment is performed. Consequently, most sequence comparison methods are designed to produce optimal alignments that take into consideration possible insertions and deletions without penalising unduly the overall homology score. This is achieved by inserting "gaps" in the sequence alignment to try to maximise local homology.

However, these more complex methods assign "gap penalties" to each gap that occurs in the alignment so that, for the same number of identical amino acids, a sequence alignment with as few gaps as possible - reflecting higher relatedness between the two compared sequences - will achieve a higher score than one with many gaps. "Affine gap costs" are typically used that charge a relatively high cost for the existence of a gap and a smaller penalty for each subsequent residue in the gap. This is the most commonly used gap scoring system. High gap penalties will of course produce optimised alignments with fewer gaps. Most alignment programs allow the gap penalties to be modified. However, it is preferred to use the default values when using such software for sequence comparisons. For example when using the GCG Wisconsin Bestfit package the default gap penalty for amino acid sequences is -12 for a gap and -4 for each extension.

Calculation of maximum % homology therefore firstly requires the production of an optimal alignment, taking into consideration gap penalties. A suitable computer program for carrying out such an alignment is the GCG Wisconsin Bestfit package (University of Wisconsin, U.S.A.; Devereux *et al.*, 1984, Nucleic Acids Research 12:387). Examples of other software than can perform sequence comparisons include,

but are not limited to, the BLAST package (see Ausubel *et al.*, 1999 ibid – Chapter 18), FASTA (Atschul *et al.*, 1990, J. Mol. Biol., 403-410) and the GENEWORKS suite of comparison tools. Both BLAST and FASTA are available for offline and online searching (see Ausubel *et al.*, 1999 ibid, pages 7-58 to 7-60). However, for some applications, it is preferred to use the GCG Bestfit program. A new tool, called BLAST 2 Sequences is also available for comparing protein and nucleotide sequence (see FEMS Microbiol Lett 1999 174(2): 247-50; FEMS Microbiol Lett 1999 177(1): 187-8 and tatiana@ncbi.nlm.nih.gov).

Although the final % homology can be measured in terms of identity, the alignment process itself is typically not based on an all-or-nothing pair comparison. Instead, a scaled similarity score matrix is generally used that assigns scores to each pairwise comparison based on chemical similarity or evolutionary distance. An example of such a matrix commonly used is the BLOSUM62 matrix - the default matrix for the BLAST suite of programs. GCG Wisconsin programs generally use either the public default values or a custom symbol comparison table if supplied (see user manual for further details). For some applications, it is preferred to use the public default values for the GCG package, or in the case of other software, the default matrix, such as BLOSUM62.

Once the software has produced an optimal alignment, it is possible to calculate % homology, preferably % sequence identity. The software typically does this as part of the sequence comparison and generates a numerical result.

The sequences may also have deletions, insertions or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent substance. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues as long as the secondary binding activity of the substance is retained. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include

leucine, isoleucine, valine, glycine, alanine, asparagine, glutamine, serine, threonine, phenylalanine, and tyrosine.

Conservative substitutions may be made, for example according to the Table below. Amino acids in the same block in the second column and preferably in the same line in the third column may be substituted for each other:

ALIPHATIC	Non-polar	G A P
		I L V
	Polar - uncharged	C S T M
		N Q
	Polar - charged	D E
		K R
AROMATIC		H F W Y

The present invention also encompasses homologous substitution (substitution and replacement are both used herein to mean the interchange of an existing amino acid residue, with an alternative residue) may occur i.e. like-for-like substitution such as basic for basic, acidic for acidic, polar for polar etc. Non-homologous substitution may also occur i.e. from one class of residue to another or alternatively involving the inclusion of unnatural amino acids such as ornithine (hereinafter referred to as Z), diaminobutyric acid ornithine (hereinafter referred to as B), norleucine ornithine (hereinafter referred to as O), pyriylalanine, thienylalanine, naphthylalanine and phenylglycine.

Replacements may also be made by unnatural amino acids include; alpha* and alpha-disubstituted* amino acids, N-alkyl amino acids*, lactic acid*, halide derivatives of natural amino acids such as trifluorotyrosine*, p-Cl-phenylalanine*, p-Br-phenylalanine*, p-I-phenylalanine*, L-allyl-glycine*, ß-alanine*, L-α-amino butyric acid*, L-γ-amino butyric acid*, L-α-amino isobutyric acid*, L-ε-amino caproic acid#, 7-amino heptanoic acid*, L-methionine sulfone#*, L-norleucine*, L-norvaline*, p-nitro-L-phenylalanine*, L-hydroxyproline#, L-thioproline*, methyl derivatives of

phenylalanine (Phe) such as 4-methyl-Phe*, pentamethyl-Phe*, L-Phe (4-amino)#, L-Tyr (methyl)*, L-Phe (4-isopropyl)*, L-Tic (1,2,3,4-tetrahydroisoquinoline-3-carboxyl acid)*, L-diaminopropionic acid # and L-Phe (4-benzyl)*. The notation * has been utilised for the purpose of the discussion above (relating to homologous or non-homologous substitution), to indicate the hydrophobic nature of the derivative whereas # has been utilised to indicate the hydrophilic nature of the derivative, #* indicates amphipathic characteristics.

Variant amino acid sequences may include suitable spacer groups that may be inserted between any two amino acid residues of the sequence including alkyl groups such as methyl, ethyl or propyl groups in addition to amino acid spacers such as glycine or β-alanine residues. A further form of variation, involves the presence of one or more amino acid residues in peptoid form, will be well understood by those skilled in the art. For the avoidance of doubt, "the peptoid form" is used to refer to variant amino acid residues wherein the α-carbon substituent group is on the residue's nitrogen atom rather than the α-carbon. Processes for preparing peptides in the peptoid form are known in the art, for example Simon RJ et al., PNAS (1992) 89(20), 9367-9371 and Horwell DC, Trends Biotechnol. (1995) 13(4), 132-134.

The term "fragment" indicates that the polypeptide comprises a fraction of the wild-type amino acid sequence. It may comprise one or more large contiguous sections of sequence or a plurality of small sections. The polypeptide may also comprise other elements of sequence, for example, it may be a fusion protein with another protein. Preferably the polypeptide comprises at least 50%, more preferably at least 65%, most preferably at least 80% of the wild-type sequence.

With respect to function, the mutant, variant, homologue or fragment should be capable of transducing adipose tissue when used to pseudotype an appropriate vector.

The viral delivery system used in the present invention may comprise nucleotide sequences that can hybridise to the nucleotide sequence presented herein (including complementary sequences of those presented herein). In a preferred aspect, the present invention covers nucleotide sequences that can hybridise to the nucleotide sequence of

the present invention under stringent conditions (e.g. 65°C and 0.1 SSC) to the nucleotide sequence presented herein (including complementary sequences of those presented herein).

A potential advantage of using the rabies glycoprotein in comparison to the VSV glycoprotein is the detailed knowledge of its toxicity to man and other animals due to the extensive use of rabies vaccines. In particular phase 1 clinical trials have been reported on the use of rabies glycoprotein expressed from a canarypox recombinant virus as a human vaccine (Fries *et al.*, 1996 Vaccine 14, 428-434), these studies concluded that the vaccine was safe for use in humans.

ADIPOSE TISSUE

As used herein, the term "adipose tissue" and particularly "white adipose tissue" means a highly specialised tissue developed particularly in mammals and birds to store fat to supply energy to the whole animal. The cells contain a single large droplet of fat, that in the nourished state, fills most of the cell. The nucleus is somewhat flattened and is in the narrow band of cytoplasm around the cell's periphery. Adipose tissue is found in many parts of the body but tends to be concentrated under the skin (subcutaneous) and around internal organs (heart and kidney). The stored fat consists principally of triacylglycerols.

Another type of adipose tissue, called "brown adipose tissue", which is a highly specialised tissue with a high content of lipid and cytochromes, is found in some animals, particularly hibernating animals and the newborn of some species. It is highly vascular and consists of small polygonal cells, each containing many separate lipid droplets and many mitochondria. Its function is thermogenesis during the arousal period after hibernation or, in the young, to provide heat before shivering has developed. It is active, also, in normal but not in obese humans. The colour is due to the high cytochrome content. Heat is generated by lipid oxidation through electron transport not coupled to oxidative phorphorylation. The uncoupling is mediated by brown fat uncoupling protein.

Adipose tissue is a large easily accessible tissues that is well vascularized. Thus, the delivery of an NOI to adipose tissue allows the rapid release of therapeutic proteins into the circulation. Adipose tissue cells are also long lived and non-dividing, thus, allowing long term expression of one of more proteins of interest (POIs) encoded by an nucleotide sequence of interest (NOI).

NOIs .

In the present invention one or more NOIs (nucleotide sequences of interest) may be delivered to a target cell *in vivo* or *in vitro*.

In accordance with the present invention, it is possible to manipulate the viral genome so that viral genes are replaced or supplemented with one or more NOIs which may be heterologous NOIs.

The term "heterologous" refers to a nucleic acid or protein sequence linked to a nucleic acid or protein sequence to which it is not naturally linked.

In the present invention, the term NOI includes any suitable nucleotide sequence, which need not necessarily be a complete naturally occurring DNA or RNA sequence. Thus, the NOI can be, for example, a synthetic RNA/DNA sequence, a recombinant RNA/DNA sequence (i.e. prepared by use of recombinant DNA techniques), a cDNA sequence or a partial genomic DNA sequence, including combinations thereof. The sequence need not be a coding region. If it is a coding region, it need not be an entire coding region. In addition, the RNA/DNA sequence can be in a sense orientation or in an anti-sense orientation. Preferably, it is in a sense orientation. Preferably, the sequence is, comprises, or is transcribed from cDNA.

In one embodiment of the present invention, a lentiviral vector system comprises at least one NOI.

A lentiviral vector genome may generally comprise LTRs at the 5' and 3' ends, suitable insertion sites for inserting one or more NOI(s), and/or a packaging signal to

enable the genome to be packaged into a vector particle in a producer cell. There may even be suitable primer binding sites and integration sites to allow reverse transcription of the vector RNA to DNA, and integration of the proviral DNA into the target cell genome. In a preferred embodiment, the lentiviral vector particle has a reverse transcription system (compatible reverse transcription and primer binding sites) and an integration system (compatible integrase and integration sites).

The NOI may encode a protein of interest ("POI"). In this way, a lentiviral delivery system could be used to examine the effect of expression of a foreign gene a target adipose tissue cell. For example, a lentiviral delivery system could be used to screen a cDNA library for a particular effect on a target adipose tissue site.

The NOI may be capable of blocking or inhibiting the expression of a gene in the target adipose tissue site. For example, the NOI may be an antisense sequence. The inhibition of gene expression using antisense technology is well known.

The NOI or a sequence derived therefrom may be capable of "knocking out" the expression of a particular gene in a target adipose tissue site. There are several "knock out" strategies known in the art. For example, the NOI may be capable of integrating in the genome of the cells of the target adipose tissue site so as to disrupt expression of the particular gene. The NOI may disrupt expression by, for example, introducing a premature stop codon, by rendering the downstream coding sequence out of frame, or by affecting the capacity of the encoded protein to fold (thereby affecting its function).

Alternatively, the NOI may be capable of enhancing or inducing ectopic expression of a gene in the target adipose tissue site. The NOI or a sequence derived therefrom may be capable of “knocking in” the expression of a particular gene.

Transduced adipose tissue cells which express a particular gene, or which lack the expression of a particular gene have applications in drug discovery and target validation. The expression system could be used to determine which genes have a desirable effect on target adipose tissue cells, such as those genes or proteins which

are able to prevent or reverse the triggering of secretory activity in the adipose tissue cells. Equally, if the inhibition or blocking of expression of a particular gene is found to have an undesirable effect on the target adipose tissue cells, this may open up possible therapeutic strategies which ensure that expression of the gene is not lost.

An NOI delivered by the viral delivery system of the present invention, such as a lentiviral vector delivery system, may be a selection gene, or a marker gene. Many different selectable markers have been used successfully in retroviral vectors. These are reviewed in "Retroviruses" (1997 Cold Spring Harbour Laboratory Press Eds: JM Coffin, SM Hughes, HE Varmus pp 444) and include, but are not limited to, the bacterial neomycin and hygromycin phosphotransferase genes which confer resistance to G418 and hygromycin respectively; a mutant mouse dihydrofolate reductase gene which confers resistance to methotrexate; the bacterial *gpt* gene which allows cells to grow in medium containing mycophenolic acid, xanthine and aminopterin; the bacterial *hisD* gene which allows cells to grow in medium without histidine but containing histidinol; the multidrug resistance gene (*mdr*) which confers resistance to a variety of drugs; and the bacterial genes which confer resistance to puromycin or phleomycin. All of these markers are dominant selectable and allow chemical selection of most cells expressing these genes.

An NOI delivered by a viral viral delivery system of the present invention, such as a lentiviral delivery system may be a therapeutic gene - in the sense that the gene itself may be capable of eliciting a therapeutic effect or it may code for a product that is capable of eliciting a therapeutic effect.

In one preferred embodiment, the NOI is capable of encoding a factor that regulates whole body metabolism.

Preferably the NOI encodes a factor that regulates body weight and lipid metabolism.

Preferably the NOI encodes a factor that regulates fat and glucose metabolism.

Preferably the NOI encodes an adipocyte complement related protein (see Fruebis et al PNAS (2001) 98: 2005-2010).

Preferably the NOI encodes a blood factor such as but not limied to erythropoietin (EPO), Factor VIII or Factor IX.

Preferably the NOI encodes an uncoupling protein (Kozak (2000) 6: 1092-1093).

In accordance with the present invention, suitable NOIs include those that are of therapeutic and/or diagnostic application such as, but not limited to: sequences encoding cytokines, chemokines, hormones, antibodies, anti-oxidant molecules, engineered immunoglobulin-like molecules, a single chain antibody, fusion proteins, enzymes, immune co-stimulatory molecules, immunomodulatory molecules, anti-sense RNA, a transdominant negative mutant of a target protein, a toxin, a conditional toxin, an antigen, a tumour suppresser protein and growth factors, membrane proteins, vasoactive proteins and peptides, anti-viral proteins and ribozymes, and derivatives thereof (such as with an associated reporter group). The NOIs may also encode pro-drug activating enzymes.

As used herein, "antibody" includes a whole immunoglobulin molecule or a part thereof or a bioisostere or a mimetic thereof or a derivative thereof or a combination thereof. Examples of a part thereof include: Fab, $F(ab)'_2$, and Fv. Examples of a bioisostere include single chain Fv (ScFv) fragments, chimeric antibodies, bifunctional antibodies.

The term "mimetic" relates to any chemical which may be a peptide, polypeptide, antibody or other organic chemical which has the same binding specificity as the antibody.

The term "derivative" as used herein includes chemical modification of an antibody. Illustrative of such modifications would be replacement of hydrogen by an alkyl, acyl, or amino group.

SCREENING METHODS

In further aspect the present invention also relates to a screening method and modulating factors isolatable by such methods, and uses for such factors.

In one embodiment, the present invention provides method for screening for modulating factors for adipose tissue cells, which comprises the following steps:

(i) providing a target adipose tissue cell;

(ii) transducing the adipose tissue cell with a cDNA library capable of encoding a plurality of candidate compounds;

(ii) monitoring the expression of the candidate compounds; and

(iii) screening for a candidate compound capable of modulating an activity of the target adipose tissue cell.

The adipose tissue cells may be transduced using a lentiviral vector system.

The cDNA library may be a ribozyme library constructed in a lentiviral vector. The ribozyme library can include but is not limited to a hammerhead ribozyme, an EGS or a group II intron ribozyme. The ribozyme library may be used to transduce cell types of interest *in vitro* and *in vivo*. These cells can then be screened for the phenotype of interest. The gene or genes affected by the ribozyme can be elucidated by PCR analysis of the ribozyme. For general teachings on ribozymes, see WO 99/41397.

The advantage of doing this with a lentivector is that it allows the transduction of primary (non-dividing) cells.

In another embodiment, the present invention provides a modulating factor for adipose tissue cells identifiable by the method as described above.

PHARMACEUTICAL COMPOSITIONS

The present invention also provides the use of a viral delivery system as defined in the first aspect of the invention in the manufacture of a pharmaceutical composition. The pharmaceutical composition may be used to deliver a NOI to a target adipose tissue cell in need of same.

The pharmaceutical composition may be used for treating an individual by gene therapy, wherein the composition comprises or is capable of producing a therapeutically effective amount of a viral vector system according to the present invention.

The method and pharmaceutical composition of the invention may be used to treat a human or animal subject. Preferably the subject is a mammalian subject. More preferably the subject is a human. Typically, a physician will determine the actual dosage which will be most suitable for an individual subject and it will vary with the age, weight and response of the particular patient.

The composition may optionally comprise a pharmaceutically acceptable carrier, diluent, excipient or adjuvant. The choice of pharmaceutical carrier, excipient or diluent can be selected with regard to the intended route of administration and standard pharmaceutical practice. The pharmaceutical compositions may comprise as (or in addition to) the carrier, excipient or diluent, any suitable binder(s), lubricant(s), suspending agent(s), coating agent(s), solubilising agent(s), and other carrier agents that may aid or increase the viral entry into the target adipose tissue site (such as for example a lipid delivery system).

Where appropriate, the pharmaceutical compositions can be administered by any one or more of: inhalation, in the form of a suppository or pessary, topically in the form of a lotion, solution, cream, ointment or dusting powder, by use of a skin patch, orally in the form of tablets containing excipients such as starch or lactose, or in capsules or ovules either alone or in admixture with excipients, or in the form of elixirs, solutions or suspensions containing flavouring or colouring agents, or they can be injected

parenterally, for example intracavernosally, intravenously, intramuscularly or subcutaneously. For parenteral administration, the compositions may be best used in the form of a sterile aqueous solution which may contain other substances, for example enough salts or monosaccharides to make the solution isotonic with blood. For buccal or sublingual administration the compositions may be administered in the form of tablets or lozenges which can be formulated in a conventional manner.

The vector system used in the present invention may conveniently be administered by direct injection into the patient.

DISEASES

The viral vector system used in the present invention is particularly useful in treating and/or preventing a disease which is associated with the death or impaired function of adipose tissue cells.

In particular, the vector system used in the present invention may be used to treat and /or prevent a disease which is associated with a derangement in the metabolism of adipose tissue cells.

In particular the present invention may be used to treat and/or prevent a condition associated with obesity, diabetes and/or whole body metabolism.

The invention will now be further described by way of Examples, which are meant to serve to assist one of ordinary skill in the art in carrying out the invention and are not intended in any way to limit the scope of the invention. The Examples refer to the Figures. In the Figures:

Figure 1 shows a photographic representation;

Figure 2 shows a photographic representation;

Figure 3 shows a photographic representation;

Figure 4 shows a photographic representation;

Figure 5 shows a photographic representation;

Figure 6 shows a photographic representation;

Figure 7 shows a photographic representation;

Figure 8 shows a plasmid map of pONY8.0Z;

Figure 9 shows a plasmid map of pONY8.0G;

Figure 10 shows a plasmid map of pONY8Z5'pos del CTS; and

Figure 11 shows a schematic representation.

In more detail:

Figure 1 shows β-galactosidase expression in the mammary fat pad tissue of nude mice, transduced with EIAV pONY8Z 5' pos del CTS vector, 14 days post injection;

Figure 2 shows β-galactosidase expression in rat gastrocnemius muscle. 14 days after the injection of VSV-G pseudotyped pONY8Z 5' pos del CTS EIAV vector;

Figure 3 shows β-galactosidase expression in mouse gastrocnemius muscle. 14 days after the injection of VSV-G pseudotyped pONY8Z 5' pos del CTS EIAV vector;

Figure 4 shows β-galactosidase expression in mouse gastrocnemius muscle. 28 days after the injection of VSV-G pseudotyped pONY8Z 5' pos del CTS EIAV vector;

Figure 5 shows β-galactosidase expression in rat gastrocnemius muscle. 28 days after the injection of VSV-G pseudotyped pONY8Zcppt EIAV vector;

Figure 6 shows β-galactosidase expression in mouse gastrocnemius muscle. 84 days after the injection of VSV-G pseudotyped pONY8Z 5' pos del CTS EIAV vector; and

Figure 7 shows β-galactosidase expression in rat gastrocnemius muscle. 84 days after the injection of VSV-G pseudotyped pONY8Z 5' pos del CTS EIAV vector.

EXAMPLES

Plasmid construction:

a) Vector plasmids

Numbering used is as of Payne *et al* 1994 (J. Gen Virol. 75:425-429). The pONY series of vectors and their pseudotyping with the different envelopes have been described previously (WO99/61639) (Mitrophanous *et al.*1999 Gene Ther 1999 6:1808-1818). pONY8.0Z (Figure 8, SEQ ID No 1) was derived from pONY4.0Z (WO99/32646) by introducing mutations which prevented expression of TAT by an 83nt deletion in the exon 2 of tat, prevented S2 expression by a 51nt deletion, prevented REV expression by deletion of a single base within exon 1 of rev and prevented expression of the N-terminal portion of gag by insertion of T in the first two ATG codons of gag, thereby changing the sequence to ATTG from ATG. With respect to the wild type EIAV sequence (Acc. No. U01866) these correspond to deletion of nt 5234-5316 inclusive, nt 5346-5396 inclusive and nt 5538. The insertion of T residues was after nt 526 and 543. pONY8.0G (Figure 9, SEQ ID No 2) was derived from pONY8.0Z by exchange of the Lac Z reporter gene for the enhanced green fluorescent protein (GFP) gene. This was done by transferring the *Sac* II – *Kpn* I fragment corresponding to the GFP gene and flanking sequences from pONY4.0G (WO99/32646) into pONY8.0Z cut with the same enzymes.

Construction of pONY8Z 5'POS del CTS

The presence of a sequence termed the central polypurine tract and central termination sequence (cPPT-see Stetor *et al.* Biochemistry. 1999 Mar 23;38(12):3656-6) improves the efficiency of gene delivery to non-dividing cells (WO 99/55892). This *cis*-acting element is located in the polymerase coding region element and can be obtained as a functional element by using PCR amplification using any plasmid which contains the

EIAV polymerase coding region (for example pONY3.1) as follows. The PCR product includes the central polypurine tract and the central termination sequence (CTS). The oligonucleotide primers used in the PCR reaction were:

EIAV cPPT POS: CAGGTTAT*TCTAGA*GTCGACGCTCTCATTACTTGTAAC

EIAV cPPT NEG: CGAATGCGT*TCTAGA*GTCGACCATGTTCACCAGGGATTTTG

Recognition sequences for *Xba*I are shown in italic and use of this enzyme facilitates insertion of the PCR product into the pONY8.0Z backbone.

Before insertion of the cPPT/CTS PCR product prepared as described above, the vector backbone was modified to remove the CTS which is already present due the presence of some EIAV *pol* sequences downstream of the reporter gene. This was achieved by subcloning the *Sal*I to *Sca*I fragment encompassing the CTS and RRE region from pONY8.0Z into pSP72 (Genbank Acc.No.X65332), prepared for ligation by digestion with *Sal*I and *Eco*RV. The CTS region was then removed by digestion with *Kpn*I and *Ppu*MI, the overhanging ends 'blunted' by T4 DNA polymerase treatment and then the ends religated. The modified EIAV vector fragment was then excised using *Sal*I and *Nhe*I and ligated into pONY8.0Z prepared for ligation by digestion with the same enzymes. This new EIAV vector was termed pONY8Z delCTS.

pONY8Z delCTS has a unique *Xba*I site which is located immediately upstream of the CMV-LacZ unit. The cPPT/CTS PCR product was digested with *Xba*I and then ligated into pONY8Z delCTS prepared for ligation by digestion with *Xba*I. Ligation into this site results in plasmids with the cPPT/CTS element in either the positive or negative senses. A clone in which the cPPT/CTS was in the positive sense (functionally active) and located to the 5'-side of the internal CMV promoter was selected and termed pONY8Z 5'POS delCTS (SEQ ID No 3 and Figure 10) The cPPT/CTS sequence was also inserted into pONY8Z delCTS, downstream of the

CMV-LacZ reporter by using the unique *Sal*I site present in the plasmid. To achieve this the cPPT/CTS PCR primer was digested with *Sal*I and then ligated with pONY8Z delCTS prepared for ligation by digestion with *Sal*I. A plasmid in which the cPPT/CTS was in the positive sense was selected and termed pONY8Z 3'POS delCTS.

<u>b) Envelope plasmids</u>

pSA91ERAwt was used for pseudotyping with rabies G. This plasmid has been described previously (WO99/61639) under the name "pSA91RbG". Briefly, pSA91ERAwt was constructed by cloning 1.7 kbp *Bgl*II rabies G fragment (strain ERA) from pSG5rabgp (Burger *et al.*, 1991 J.Gen. Virol. 72. 359-367) into pSA91, a derivative of pGW1HG (Soneoka *et al* 1995 Nucl. Acids Res. 23: 628-633) from which the *gpt* gene has been removed by digestion with *Bam*HI and re-ligation. This construct, pSA91ERAwt, allows expression of rabies G from the human cytomegalovirus (HCMV) immediate early gene promoter-enhancer.

pRV67 was used for pseudotyping with VSV-G. pRV67 (described in WO99/61639) is a VSV-G expression plasmid in which VSV-G was expressed under the control of human cytomegalovirus promoter/enhancer, in place of rabies G in pSA91ERAwt.

<u>Production and Assay of Vectors:</u> Vector stocks were generated by calcium-phosphate transfection of human kidney 293T cells plated on 10 cm dishes with 16 μg of vector plasmid, 16 μg of gag/pol plasmid and 8 μg of Rabies G envelope plasmid. 36-48 h after transfection, supernatants were filtered (0.45 μm) aliquoted and stored at -70°C. Concentrated vector preparations were made by initial low speed centrifugation 6 000 x g (JLA-10.500 for 16 hours at 4 °C followed by ultracentrifugation at 20 000 rpm (SW40Ti rotor) for 90 min, at 4 °C. The virus was resuspended in PBS for 3-4 h aliquoted and stored at -70 °C. Transduction was carried out in the presence of polybrene (8 μg/ml).

Gene transfer with EIAV vectors into adipose tissue and muscle cells.

Transduction of adipose tissue.

40μl of VSV-G pseudotyped EIAV pONY8Z 5' pos del CTS vector containing 4 x 10^7 TU was injected into the mammary fat pads of six nude mice and into the fatty tissue near to the epididymius of six nude rats. Controls of three mice and three rats were used where 40μl of the buffer used to re-suspend the virus was injected into the appropriate sites. Two mice and two rats were culled on days 14, 28 and 84. A single control animal was culled on each day. The tissues were harvested and snap frozen in liquid nitrogen. These were then sectioned and stained for β-galactosidase activity.

Results I

Significant staining was observed in the mouse mammary fat pad samples throughout the duration of the experiment. Images of sections taken after 14 days after the vectors were injected are shown in figure 1. No staining was observed in any of the rats.

Transduction of skeletal muscle.

10μl aliquots of VSV-G pseudotyped EIAV pONY8Z 5' pos del CTS vector was injected into four different sites in the gastrocnemius muscle of the left legs of six nude mice and six nude rats. This is a dose of 4 x 10^7 TU per animal. Controls of three mice and three rats were used where 10 μl aliquots of the buffer used to re-suspend the virus were injected into the appropriate sites. Two mice and two rats were culled on days 14, 28 and 84. A single control animal was culled on each day. The tissues were harvested and snap frozen in liquid nitrogen. These were then sectioned and stained for β-galactosidase activity.

Results II

Significant staining was observed in all of the test mice examined and in 5 out of the six rats examined.

Discussion

The results demonstrate that long term expression may be maintained in adipose and skeletal muscle cells using minimal EIAV vectors.

Both adipose tissue and skeletal muscle tissue have features that make them suitable to use as sites to manufacture therapeutically useful proteins. By way of example, adipose tissue has a major endocrine role in addition to its triglyceride storage role. The most important endocrine role of adipose tissue is probably the secretion of leptin. However other factors such as sex steroids and glucocorticoids, peptide hormone precursors (eg angiotensinogen), complement factors, pro-inflammatory cytokines, interleukin 6, transforming growth factor-beta, tissue factor, plasminogen activator inhibitor-1 Aipo Q and adiponectin are also secreted. Aberrant function of this tissue is associated with diseases such as diabetes (related to low levels of leptin secretion). Thus the regulation or alteration of these secretory functions by gene delivery may be used to treat a varied range of diseases.

Consequently, the use of a viral vector system, such as a lentiviral vector system (such as EIAV and HIV lentiviral vectors systems) may be used to facilitate studies into the ways in which adipose tissue secretions are involved in disease phenotypes. These vectors may be used to selectively over or under express identified targets or to introduce cDNA or ribozyme libraries to identify new targets for pharmaceutical or gene delivery treatments.

All publications mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described methods and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention

which are obvious to those skilled in chemistry, biology or related fields are intended to be within the scope of the following claims.

SEQUENCE LISTINGS

SEQ ID NO 1

PONY8Z

AGATCTTGAATAATAAAATGTGTGTTTGTCCGAAATACGCGTTTTGAGATTTCTGTCGCC
GACTAAATTCATGTCGCGCGATAGTGGTGTTTATCGCCGATAGAGATGGCGATATTGGAA
AAATTGATATTTGAAAATATGGCATATTGAAAATGTCGCCGATGTGAGTTTCTGTGTAAC
TGATATCGCCATTTTTCCAAAAGTGATTTTTGGGCATACGCGATATCTGGCGATAGCGCT
TATATCGTTTACGGGGGATGGCGATAGACGACTTTGGTGACTTGGGCGATTCTGTGTGTC
GCAAATATCGCAGTTTCGATATAGGTGACAGACGATATGAGGCTATATCGCCGATAGAGG
CGACATCAAGCTGGCACATGGCCAATGCATATCGATCTATACATTGAATCAATATTGGCC
ATTAGCCATATTATTCATTGGTTATATAGCATAAATCAATATTGGCTATTGGCCATTGCA
TACGTTGTATCCATATCGTAATATGTACATTTATATTGGCTCATGTCCAACATTACCGCC
ATGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCA
TAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACC
GCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAAT
AGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGT
ACATCAAGTGTATCATATGCCAAGTCCGCCCCCTATTGACGTCAATGACGGTAAATGGCC
CGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTCCTACTTGGCAGTACATCTA
CGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACACCAATGGGCGTGG
ATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTT
GTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTGCGATCGCCCGCC
CCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCGT
TTAGTGAACCGGGCACTCAGATTCTGCGGTCTGAGTCCCTTCTCTGCTGGGCTGAAAAGG
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SEQ ID NO 3 pONY 8Z 5' pol del CTS

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CLAIMS

1. The use of a viral vector system to transduce a target adipose tissue site.

2. The use of a viral vector system according to claim 1 wherein the viral vector is pseudotyped with a nucleotide sequence that encodes at least a part of an env protein.

3. The use of a viral vector system according to claim 1 or claim 2 wherein the env protein is a Rabies G protein or a mutant, variant, homologue or fragment thereof.

4. The use of a viral vector system according to claim 1 or claim 2 wherein the env protein is a VSV-G protein or a mutant, variant, homologue or fragment thereof.

5. The use according to any one of the preceding claims, wherein the viral vector system is derivable from the group selected from a lentivirus, an adenovirus, an adeno-associated virus, a pox virus, a herpes virus and a baculovirus.

6. The use according to claim 5, wherein the lentiviral vector system is derivable from EIAV or HIV.

7. The use according to any one of the preceding claims, wherein the viral vector system comprises at least one NOI.

8. The use according to any one of the preceding claims, wherein the NOI is a selection gene, a marker gene, a therapeutic gene, an antisense sequence or a cDNA library.

9. The use according to any one of the preceding claims, wherein the NOI is capable of blocking or inhibiting the expression of a gene in a target cell.

10. The use according to any one of the preceding claims, wherein at least part of the NOI is capable of integrating in the genome of a target cell.

11. The use according to any one of the preceding claims, wherein the NOI has a therapeutic effect or codes for a protein that has a therapeutic effect.

12. The use according to any one of the preceding claims, wherein the NOI is capable of encoding a protein of interest ("POI").

13. The use of a viral vector system as defined in any one of claims 1 to 12, in the manufacture of a pharmaceutical composition to treat and/or prevent a disease in a subject.

14. A method of treating and/or preventing a disease in a subject in need of same, said method comprising the step of using a viral vector system as defined in any one of claims 1 to 12 to transduce a target adipose tissue site.

15. A method according to claim 14, to treat and/or prevent a disease which is associated with a derangement in the metabolism of adipose tissue.

16. A method according to claim 13 or 15, to treat and/or prevent obesity and/or diabetes.

17. A method for analysing the effect of a POI in a target adipose tissue site comprising the step of using a viral vector system as defined in claim 12.

18. A method for analysing the function of a gene, or a protein encoded by a gene, in a target cell, which method comprises the step of inhibiting or blocking the expression of the gene using a viral vector system as defined in claim 9.

19. A target adipose tissue cell transduced with a viral vector system as defined in any one of claims 1 to 12.

20. The use of a target adipose tissue cell according to claim 19 in the manufacture of a medicament for use in the prevention and/or treatment of a condition associated with adipose tissue metabolism.

21. A method for treating and/or preventing a disease in a subject in need of same, said method comprising the step of transplanting a target adipose tissue cell according to claim 20 into said subject.

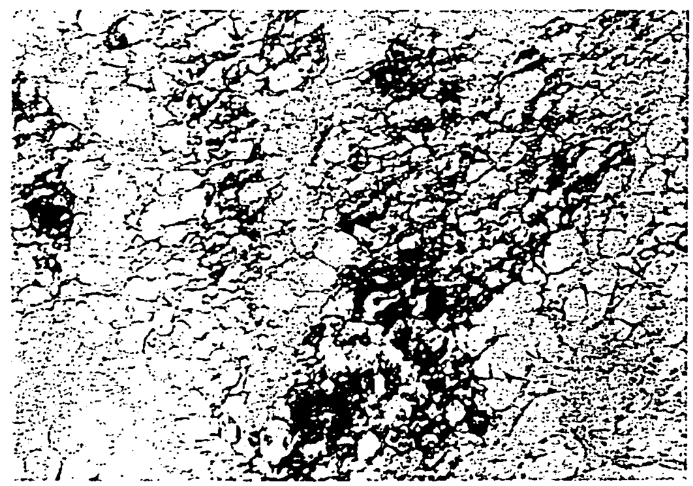
ABSTRACT

VECTOR SYSTEM

The invention provides the use of a viral vector system to transduce a target adipose tissue site. The invention also provides a method of treating and/or preventing a disease in a subject and use of a viral vector system in the manufacture of a pharmaceutical composition to transduce a target adipose tissue site wherein the disease is associated with a derangement in the metabolism of adipose tissue.

β-galactosidase expression in the mammary fat pad tissue of nude mice, transduced with EIAV pONY 8Z 5' pos del CTS vector, 14 days post injection.

Section 1



4 x magnification

10x magnification

Section 2

Figure 1

β-galactosidase expression in rat gastrocnemius muscle. 14 days after the injection of VSV-G pseudotyped EIAV pONY 8Z 5' pos del CTS vector.

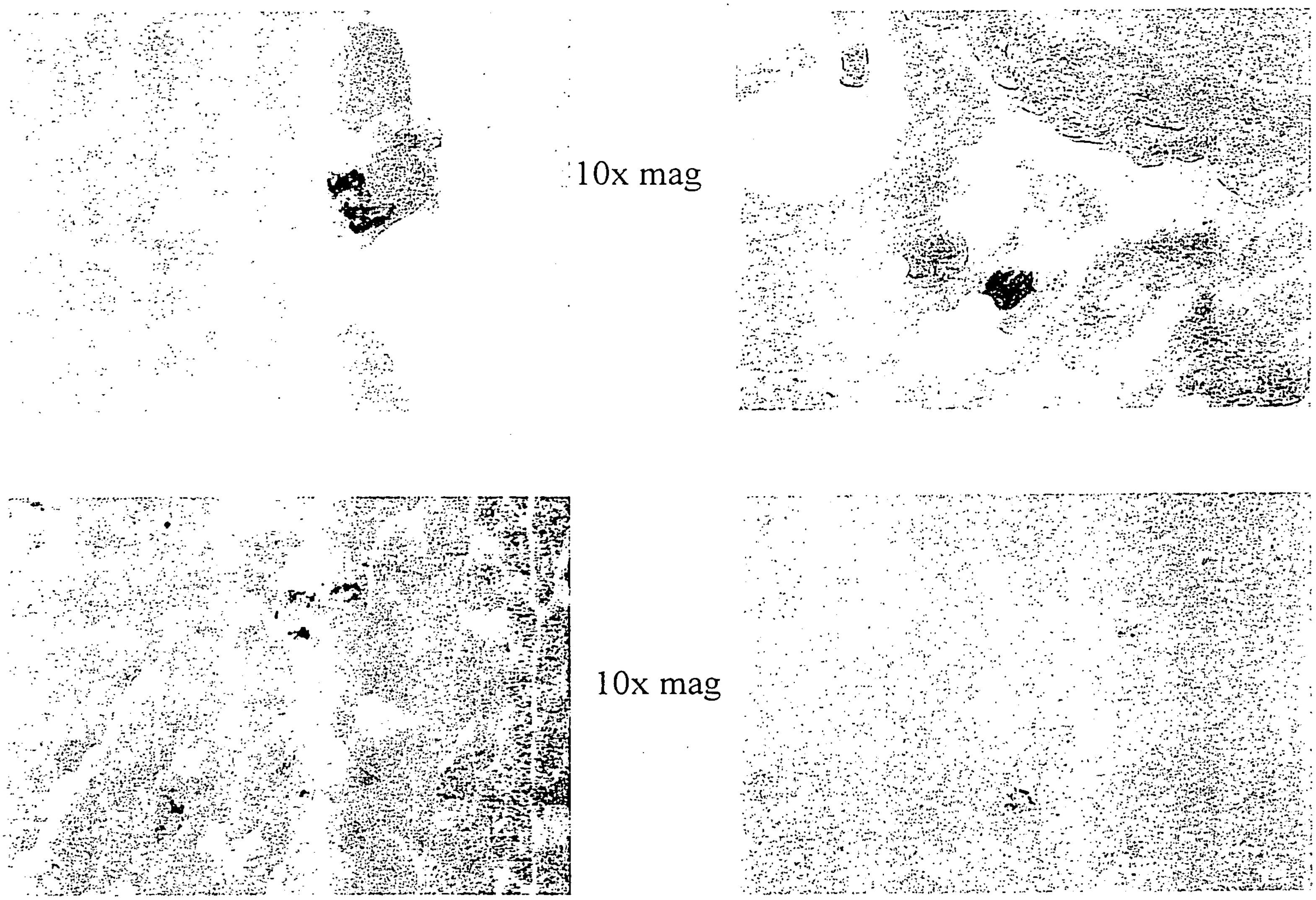


Figure 2

β-galactosidase expression in mouse gastrocnemius muscle. 14 days after the injection of VSV-G pseudotyped EIAV pONY 8Z 5' pos del CTS vector.

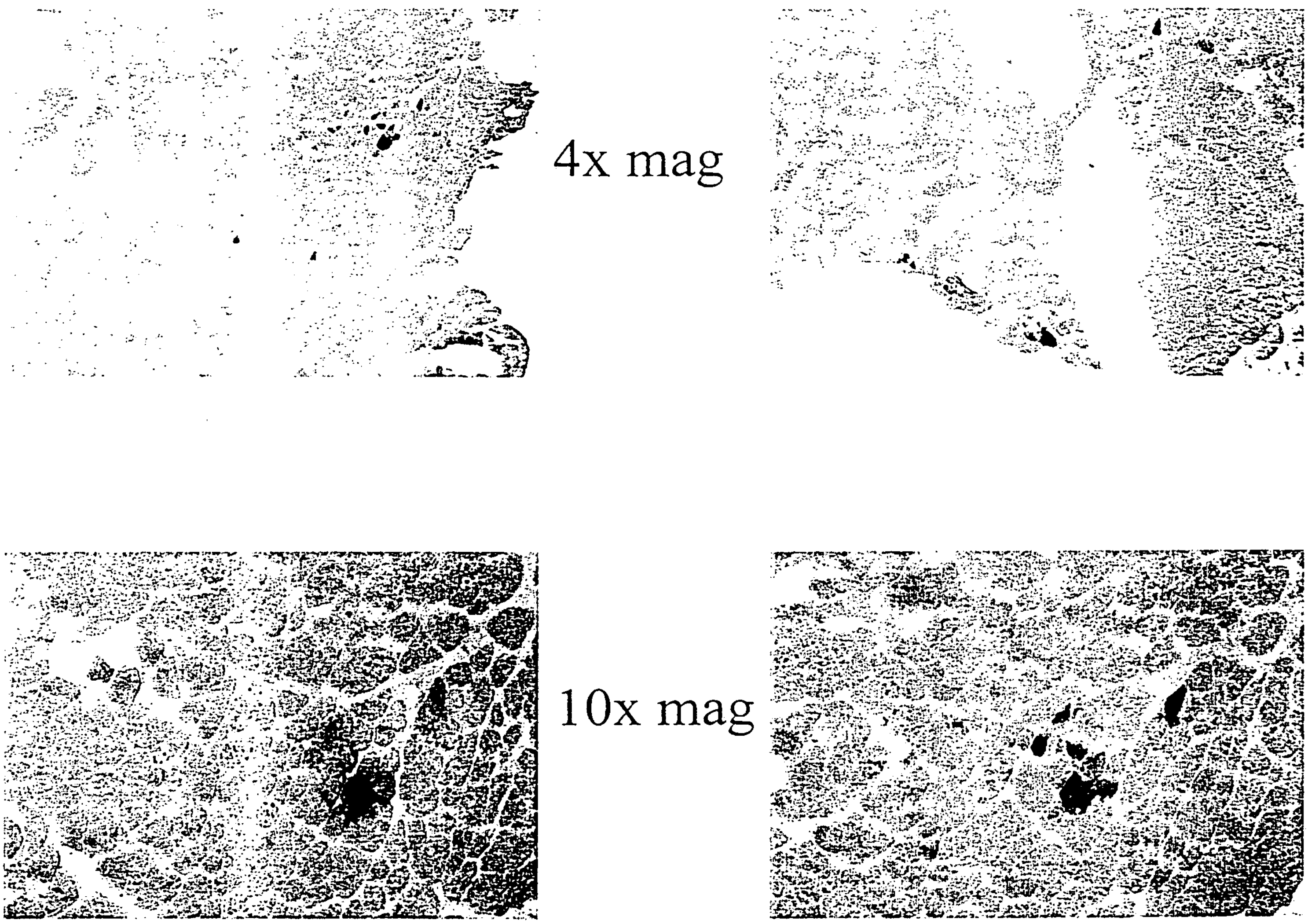


Figure 3

β-galactosidase expression in mouse gastrocnemius muscle. 28 days after the injection of VSV-G pseudotyped EIAV pONY 8Z 5' pos del CTS vector.

4x

10x

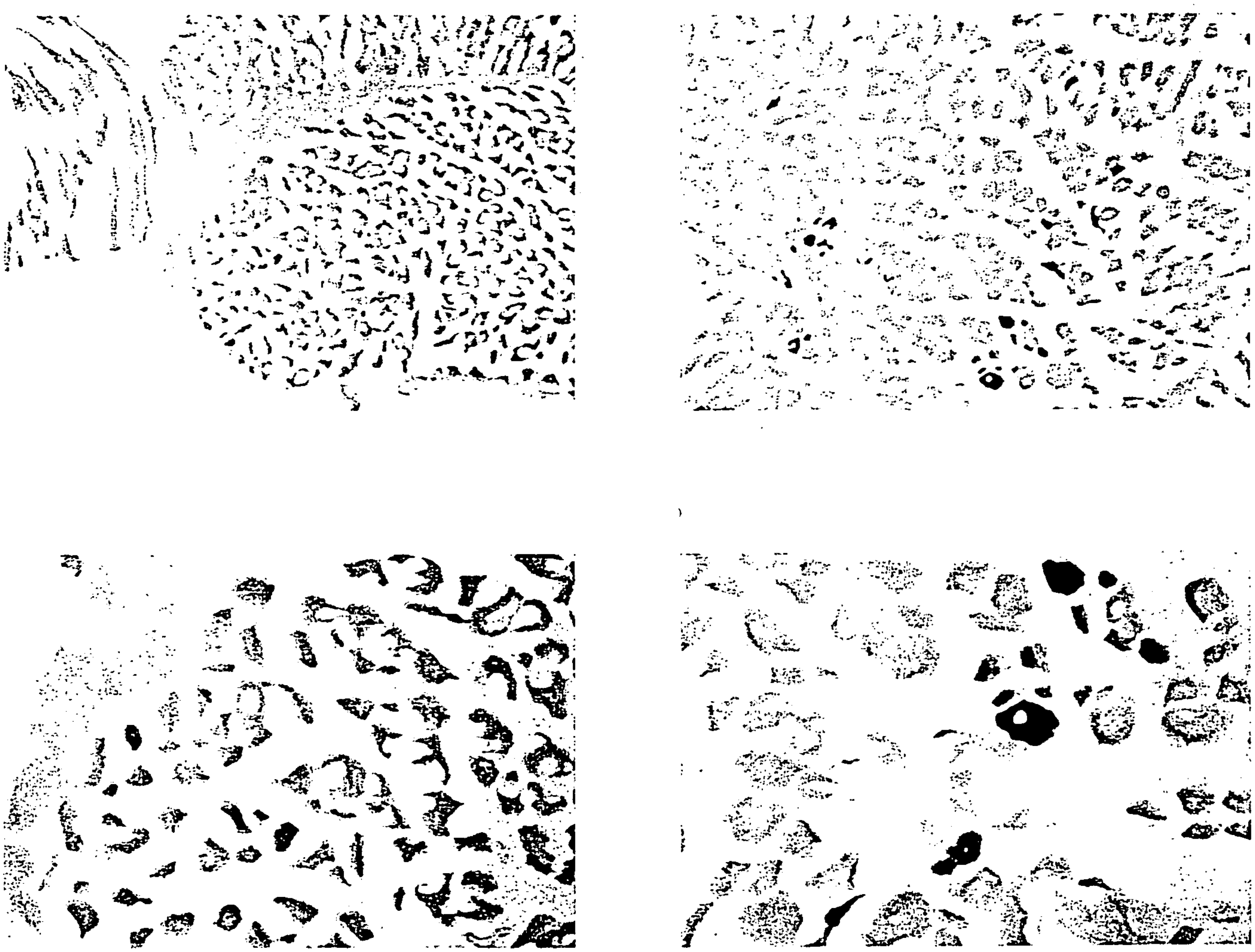
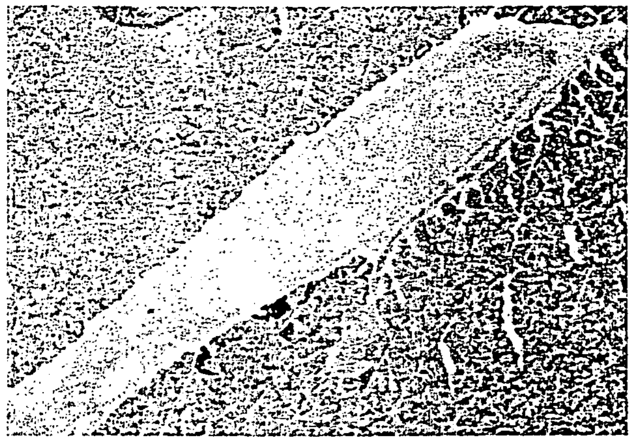


Figure 4

Staining could be found in both of the two animals examined.

β-galactosidase expression in rat gastrocnemius muscle. 28 days after the injection of VSV-G pseudotyped EIAV pONY 8Z 5' pos del CTS vector.

4x



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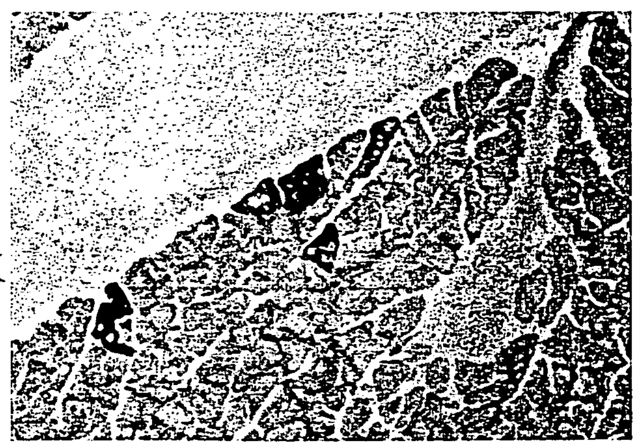

Figure 5

Staining could only be found in one of the two animals examined.

β-galactosidase expression in mouse gastrocnemius muscle. 84 days after the injection of VSV-G pseudotyped EIAV pONY 8Z 5' pos del CTS vector.

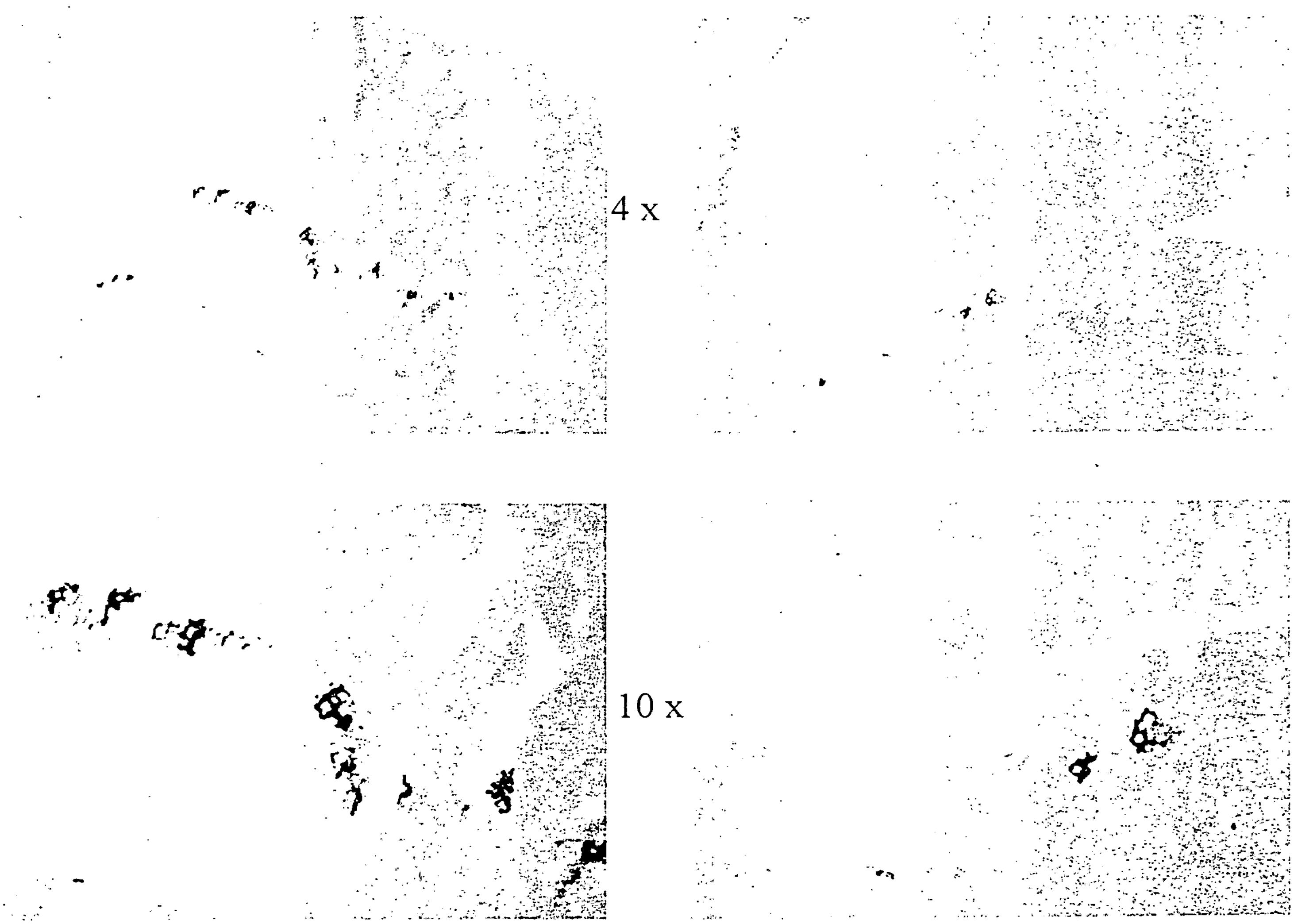

Figure 6

Staining could be found in both of the two animals examined.

β-galactosidase expression in rat gastrocnemius muscle. 84 days after the injection of VSV-G pseudotyped EIAV pONY 8Z 5' pos del CTS vector.

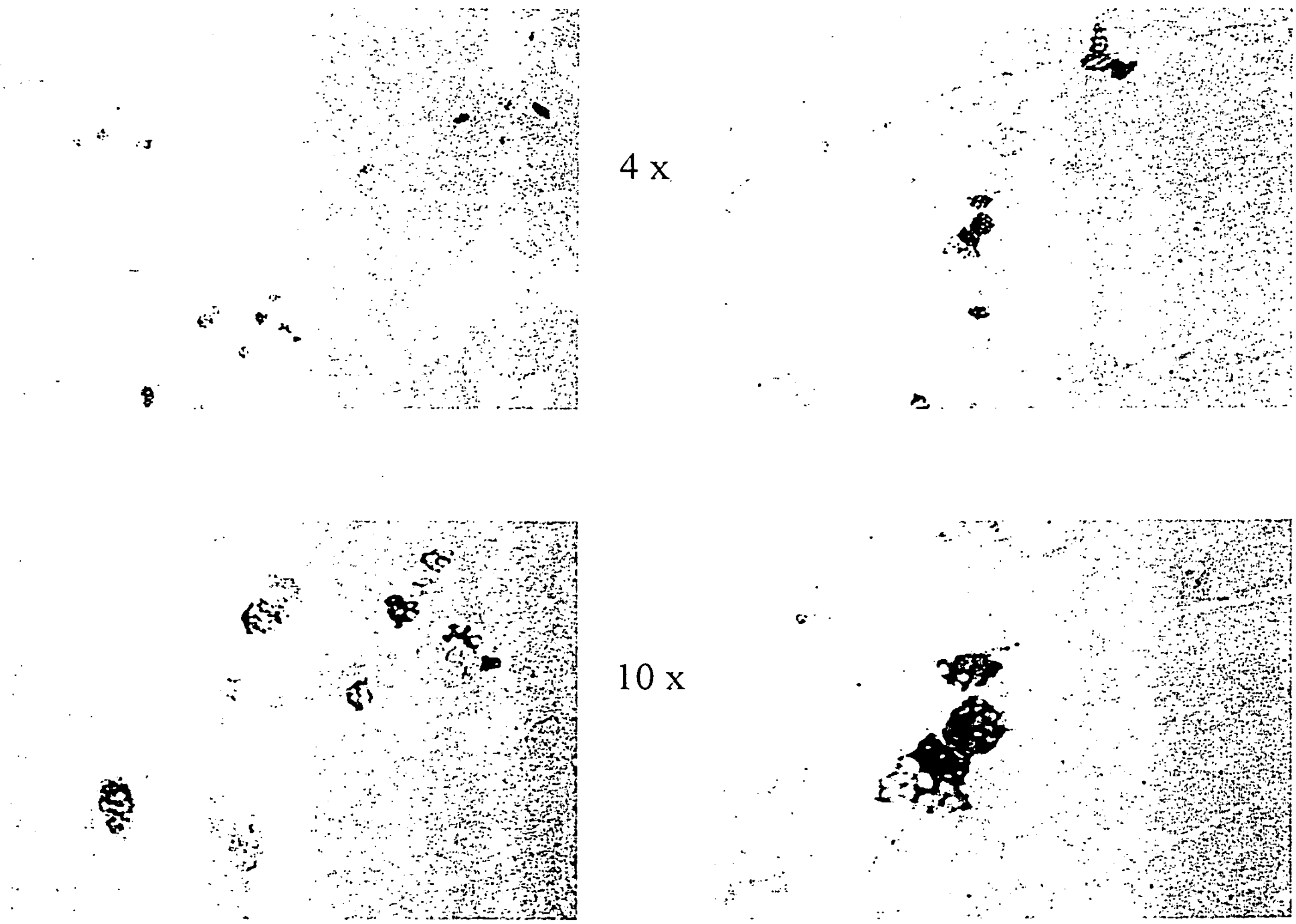

Figure 7

Staining could be found in both of the two animals examined.

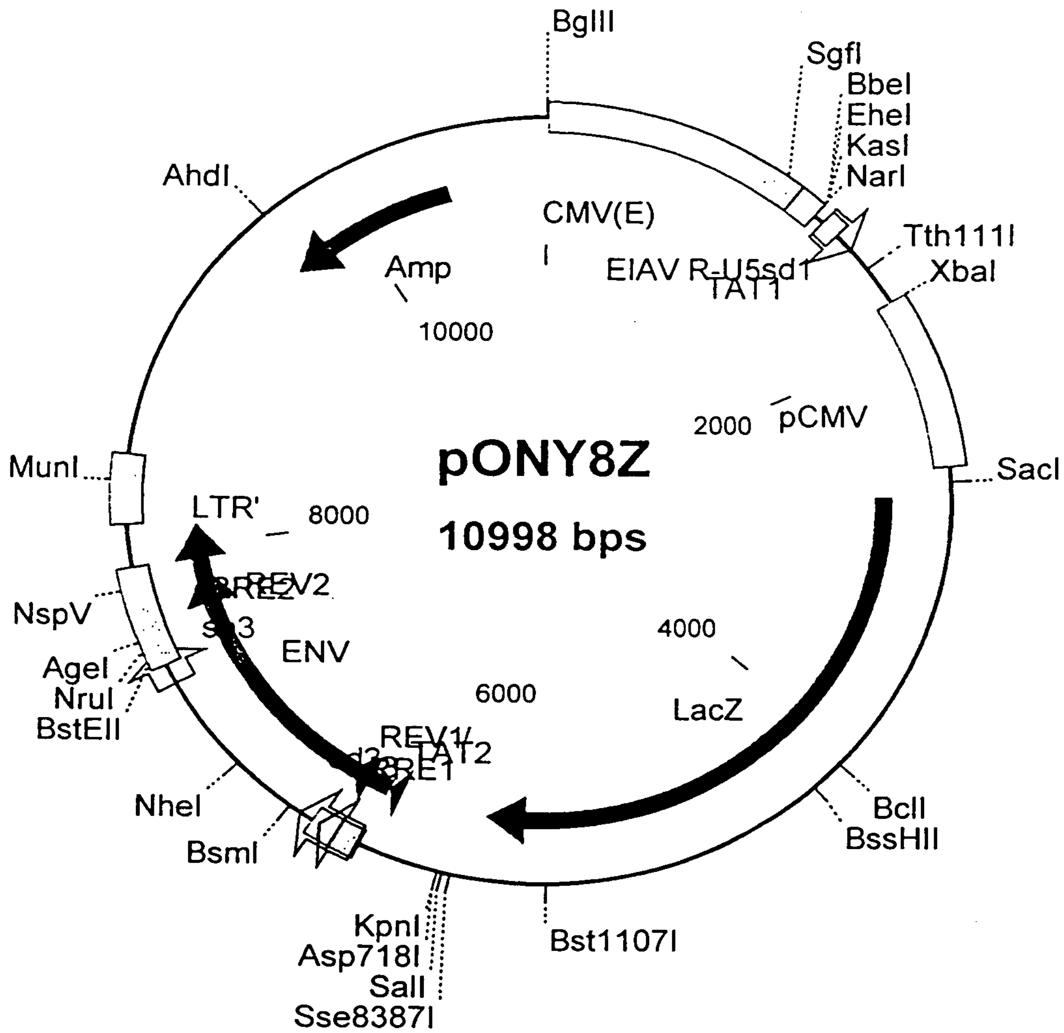
BglII
SgfI
BbeI
EheI
KasI
NarI
Tth111I
XbaI
SacII
BclI
BssHII
Bst1107I
KpnI
Asp718I
SalI
Sse8387I
BsmI
NheI
BstEII
NruI
AgeI
NspV
MunI
AhdI
CMV(E)
Amp
EIAV R-U5sd1
TAT1
10000
2000
pCMV
pONY8Z
10998 bps
LTR'
8000
REV2
RRE2
ENV
4000
6000
LacZ
REV1
TAT2
RRE1

Figure 8

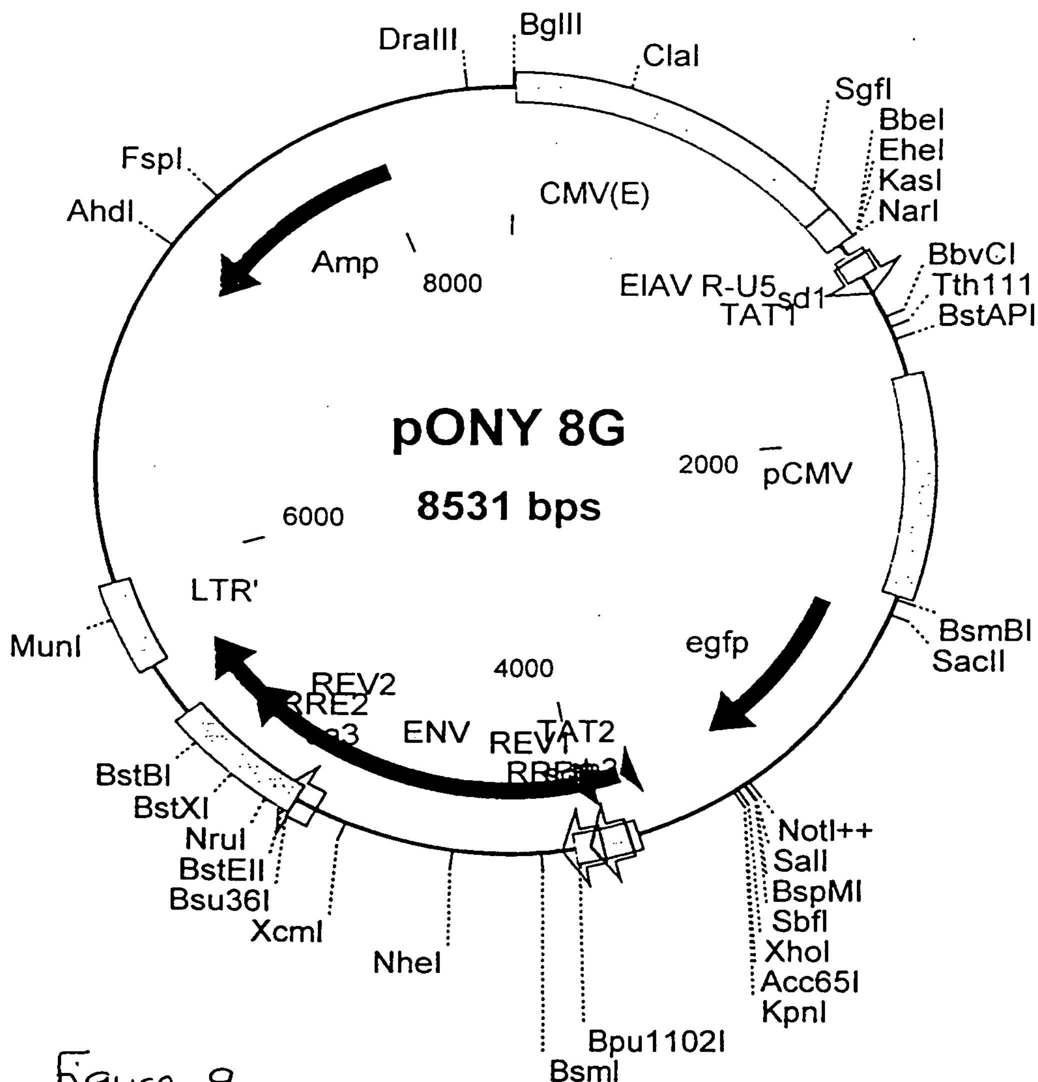
DraIII
BglII
ClaI
SgfI
BbeI
EheI
KasI
NarI
BbvCI
Tth111I
BstAPI
FspI
AhdI
CMV(E)
Amp
8000
EIAV R-U5
sd1
TAT1
pONY 8G
8531 bps
2000
pCMV
6000
LTR'
BsmBI
SacII
egfp
MunI
4000
REV2
RRE2
ENV
REV1
TAT2
BstBI
BstXI
NruI
BstEII
Bsu36I
XcmI
NheI
NotI++
SalI
BspMI
SbfI
XhoI
Acc65I
KpnI
Bpu1102I
BsmI

Figure 9

pONY8Z 5'POS delCTS

11019 bps

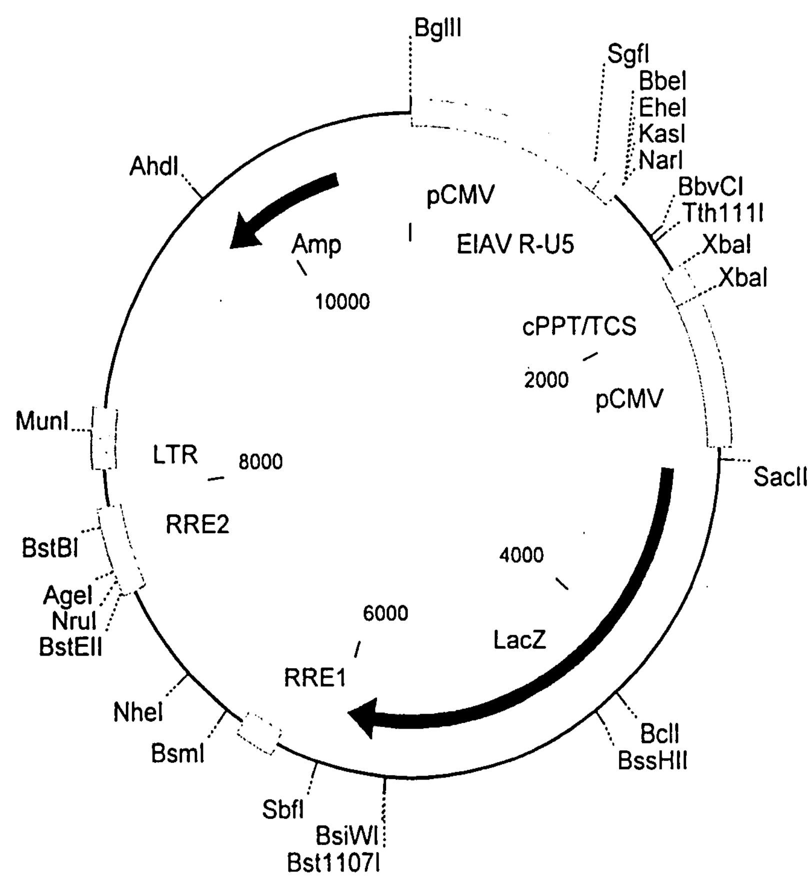

Figure 10

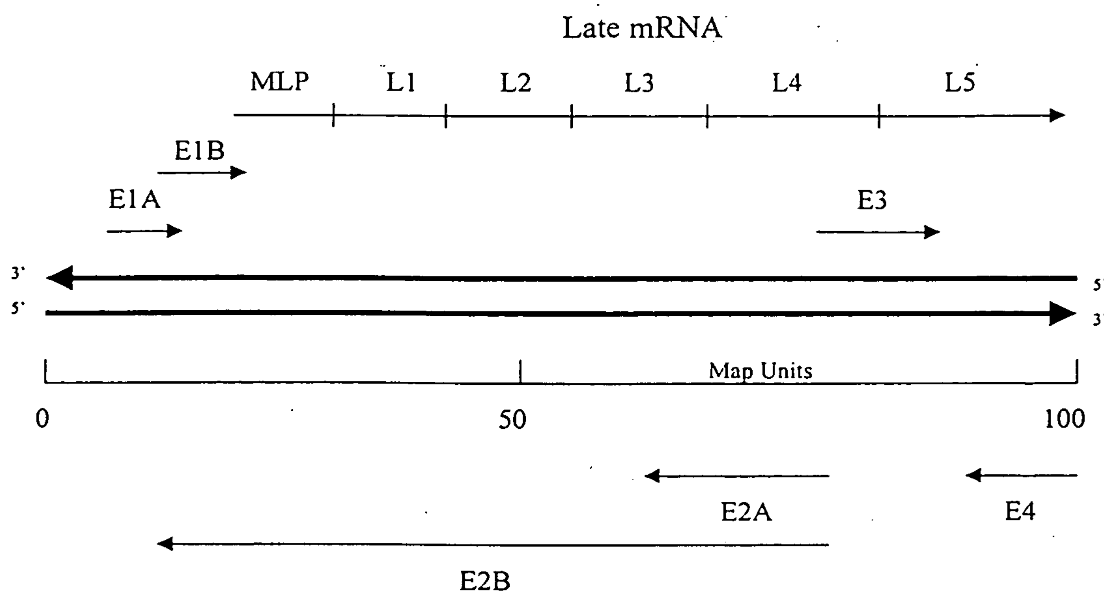
Late mRNA
MLP
L1
L2
L3
L4
L5
E1B
E1A
E3
3'
5'
5'
3'
Map Units
0
50
100
E2A
E4
E2B

Figure 11